

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2003, 08:32:46 ; Search time 207.841 Seconds

(without alignments)  
8065.662 Million cell updates/sec

Title: US-08-951-733-19

Perfect score: 3798

Sequence: 1 CCACGCTCGGGCAGCGCT.....GGAATAGTCCATCCCTGAT 3798

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	3784.4	99.6	4015	3	US-08-974-549A-1
3	3784.4	99.6	4015	3	US-08-854-050-224
4	3784.4	99.6	4015	4	US-09-430-323-224
5	3784.4	99.6	4015	4	US-09-572-423B-3
6	3784.4	99.6	4015	4	US-09-128-354-1
7	3784.4	99.6	4015	4	US-09-675-321-1
8	3784.4	99.6	4015	4	US-09-052-919-1
9	3784.4	99.6	4015	4	US-08-912-951-1
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15	3618.6	95.3	4029	4	US-09-430-323-173
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c 45 67.6 1.8 90 3 US-08-974-549A-697

## ALIGNMENTS

### RESULT 1

US-08-851-843A-224  
; Sequence 224, Application US/08851843A  
; Patent No. 6093809  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: No. 6093809el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/851.843A  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 224:

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Sequence 6, Appli  
Sequence 6, Appli  
Sequence 1, Appli  
Sequence 30, Appl  
Sequence 62, Appl  
Sequence 8, Appli  
Sequence 62, Appl  
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Sequence 7, Appli  
Sequence 11, Appl  
Sequence 697, App

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; LENGTH: 4015 base pairs									
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; STRANDEDNESS: single									
; TOPOLOGY: linear									
; MOLECULE TYPE: cDNA									
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; OTHER INFORMATION: component"									
US-08-851-843A-224									
Query Match									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	13	GCAGCGTGCCTCTGTCGCGACAGTGGGAAAGCCCTGGCCCGCGCCACCCCGCGATGCC	72						
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QY	73	CGCGCTCCCGCTGCGAGCGCGCTCCCTGCTGCGACGACCTACCGGAGGTGCT	132						
Db	61	CGCGCTCCCGCTGCGAGCGCGCTCCCTGCTGCGACGACCTACCGGAGGTGCT	120						
QY	133	CGCGTGCACAGTTTCGTCGCGCGCTGGGGCCCGAGGCTTGGTGCACGCGGG	192						
Db	121	CGCGTGCACAGTTTCGTCGCGCGCTGGGGCCCGAGGCTTGGTGCACGCGGG	180						
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QY	253	ACGGCGCGCCCGCGCGCTCTCTCCGCGAGTGTCTGCTGAGAGGAGTGTGGC	312						
Db	241	ACGGCGCGCCCGCGCGCTCTCTCCGCGAGTGTCTGCTGAGAGGAGTGTGGC	300						
QY	313	CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCGAAGACGTGTGGCTTCGGCTTCGC	372						
Db	301	CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCGAAGACGTGTGGCTTCGGCTTCGC	360						
QY	373	GCTGTGACAGGGCGCGGGGGCGCCCGAGGCTTACACGAGCTGCGGAGCTA	432						
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QY	433	CCTGCCAACAGGTGACGACGACATGCGGGGAGCGGGCGTGGGGCTGTGCTCGG	492						
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QY	493	CCGCTGGGGACAGCTGCTGGTTTACCTGCTGCGACGCTCGCGCTCTTTTGTCTGTT	552						
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QY	553	GGCTCCAGCTGCGGCTACAGAGTGTGGGGCGCGCGCTGTACACGCTGCGGCTGCCAC	612						
Db	541	GGCTCCAGCTGCGGCTACAGAGTGTGGGGCGCGCGCTGTACACGCTGCGGCTGCCAC	600						
QY	613	TCAGCGCGCGCGCGCGCACAGCTAGTGGACCGCGAAGGCTCTGGGATGCGAACGGCG	672						
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Db	661	CTGGAACCATAGCTGACGGAGCGCGGGTCCCTGCGGCTTGCAGCGCGGGTGGCAG	720						
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QY	853	CGTGGACCGAGTGACCGTGTGTTCTGTGTGTGTCACTGTCCAGACCGCGCGAAGAC	912
Db	841	CGTGGACCGAGTGACCGTGTGTTCTGTGTGTGTCACTGTCCAGACCGCGCGAAGAC	900
QY	913	CACCTCTTTTGGAGGTGCGCTCTGTGGACGCGGCACCTCCACCCATCCGTGGGCGGCA	972
Db	901	CACCTCTTTTGGAGGTGCGCTCTGTGGACGCGGCACCTCCACCCATCCGTGGGCGGCA	960
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QY	1033	CCCGTGTACGCGGACGACCTTCTCTACTCTCAGCGCAACAGGAGCAGCTGCG	1092
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QY	1333	AGCGCGTCTCTGTGCGCGGAGACCCAGGGCTCTGTGGGGCCCCCGAGGAGAGGA	1392
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Db	1501	CAACGAACCGCTTCTCAGGAACCAAGAAATTCATCTCCCTGGGGAAGCATGCCAA	1560
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Db	1621	GAGCCCCAGGGTGGCTGTGTCGGCGCAGACGACCGTCTGCTGAGGAGATCCTGCG	1680
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Db	1801	CAAGTTGCAAGCATTTGGAATCAGACAGCTTTGAAGAGGTGACGTGCGGGAGCTGTC	1860
QY	1873	GGAACGAGGCTCAGGAGCATCGGGAAGCCAGGCCCTGCTGACGTCCAGACTCCG	1932
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QY 1933 CTTTCATCCCAAGCCTGACGGCTGCGCGGATTTGTGAACATGAGCTACGTCGTGGAGC 1992  
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QY 1993 CAGAACCTTCGCGAGAGAAAAGAGGGCGGAGCGCTCTCACTCGAGGGTGAAGGACACTGTT 2052  
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QY 2953 CGGCTTCAAGGCTGGGAGAACATGCTGCTGCAAACTCTTTGGGTCTTGGGCTGAAGT 3012  
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Db 3301 GACTGACACCGTGTCACTTACCTGACCTGCTCTGGGTCTACTCAGGACAGCCAGAGCCA 3360  
QY 3373 GCTGAGTGGAGTCCCGGGAGCGCTGACTGCTGAGGCGCGAGCGCCAGCCCGC 3432  
Db 3361 GCTGAGTGGAGTCCCGGGAGCGCTGACTGCTGAGGCGCGAGCGCCAGCCCGC 3420  
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## RESULT 2

US-08-974-549A-1  
; Sequence 1, Application US/08974549A  
; Patent No. 6166178  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin B.  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Crew LLP

;; STREET: Two Embarcadero Center, Eighth Floor  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94111-3834  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/974,549A  
;; FILING DATE: 19-NOV-1997  
;; CLASSIFICATION: 536  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/724,643  
;; FILING DATE: 01-OCT-1996  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/844,419  
;; FILING DATE: 18-APR-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/846,017  
;; FILING DATE: 25-APR-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/851,843  
;; FILING DATE: 06-MAY-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/854,050  
;; FILING DATE: 09-MAY-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/911,312  
;; FILING DATE: 14-AUG-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/912,951  
;; FILING DATE: 14-AUG-1997  
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;; APPLICATION NUMBER: US 08/915,503  
;; FILING DATE: 14-AUG-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: WO PCT/US97/17618  
;; FILING DATE: 01-OCT-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: WO PCT/US97/17885  
;; FILING DATE: 01-OCT-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Apple, Randolph Ted  
;; REGISTRATION NUMBER: 36,429  
;; REFERENCE/DOCKET NUMBER: 015389-002610US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4015 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
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US-08-974-549A-1

Query Match 99.6%; Score 3784.4; DB 3; Length 4015;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 GCAGCGTGGCTCTGCTGGCAGCTGGGAGCCCTGGCCCCGGCCACCCCGCGGATGCC 72  
|||||

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RESULT 3

US-08-854-050-224  
; Sequence 224, Application US/08854050  
; Patent No. 6261836

GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: No. 6261836el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/854,050  
; FILING DATE: 09-MAY-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997

; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-0029300S  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 224:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4015 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
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; OTHER INFORMATION: /product= "hprt"  
; OTHER INFORMATION: /note= "human telomerase reverse  
; OTHER INFORMATION: transcriptase (hTERT) catalytic protein  
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Query Match 99.6%; Score 3784.4; DB 3; Length 4015;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 133 GCGCGTGGCCAGTGTGTCGCGGCGCTGGGGGCCCCAGGGCTGCGGCGTGGTGCAGGCGG 192  
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Db 181 GGACCGCGGCGCTTTCCGCGCGCTGGTGGCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240  
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QY 373 GCTGTGGACGGGGCGCGCGGGGGCCCCCCCCAGGCGCTTCCAGCAGCGTGGCAGTGA 432  
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RESULT 4  
US-09-430-323-224  
; Sequence 224, Application US/09430323  
; Patent No. 6309867  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. 6309867el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/430,323  
; FILING DATE: 29-Oct-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 224:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4015 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
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Query Match 99.6%; Score 3784.4; DB 4; Length 4015;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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QY	133	GC	GC	GCCTGCGCACGTTCTGTCGGCG	CCCTGSGGCCACAGGCTGCGCGCT	GTGTCAGCGCG	192
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QY	121	GC	GC	GCCTGCGCACGTTCTGTCGGCG	CCCTGSGGCCACAGGCTGCGCGCT	GTGTCAGCGCG	180
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QY	193	GG	AC	CCCGCGCGCTTTCGCGCGCT	TGSGGCCAGTGTGCTGCGCTGCGCT	TGGGAGCG	252
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QY	181	GG	AC	CCCGCGCGCTTTCGCGCGCT	TGSGGCCAGTGTGCTGCGCTGCGCT	TGGGAGCG	240
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QY	253	AC	GC	CGCGCCCGCCCGCCCGCTCT	TCGCGCAGGTGTCTGCTGAAGAG	CTGTGTGGC	312
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QY	241	AC	GC	CGCGCCCGCCCGCCCGCTCT	TCGCGCAGGTGTCTGCTGAAGAG	CTGTGTGGC	300
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QY	313	CC	GAG	TGCTGCAGAGGCTGTGCGAGCG	CGCGCGGAAGCTGTGTCGCCCT	TTCGCTTCGC	372
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QY	301	CC	GAG	TGCTGCAGAGGCTGTGCGAGCG	CGCGGAAGCTGTGTCGCCCT	TTCGCTTCGC	360
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QY	373	GT	CT	GCTGTGAGGGGCGCGGGGCC	CCCCCGAGGCCCTTACCACCA	GCAGCTTGGCAGCTA	432
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QY	361	GT	CT	GCTGTGAGGGGCGCGGGGCC	CCCCCGAGGCCCTTACCACCA	GCAGCTTGGCAGCTA	420
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QY	433	CT	TG	CGCCCAACACAGGTGACGACG	ACATGCGGGGAGCGGGGCTGT	GTGTGTGCG	492
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QY	421	CT	TG	CGCCCAACACAGGTGACGACG	ACATGCGGGGAGCGGGGCTGT	GTGTGTGCG	480
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QY	493	CC	GC	GCTGGGGACGACGTGTGTTCA	CTGTCTGCTGGACGCTGCGCGCT	CTTTGTGTGCGT	552
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QY	481	CC	GC	GCTGGGGACGACGTGTGTTCA	CTGTCTGCTGGACGCTGCGCGCT	CTTTGTGTGCGT	540
DB							
QY	553	GG	CT	CCAGCTGCGCCTACCAAGTGT	GCGGGCGCGCTGTACCA	GCCTCGGCGTGCAC	612
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QY	541	GG	CT	CCAGCTGCGCCTACCAAGTGT	GCGGGCGCGCTGTACCA	GCCTCGGCGTGCAC	600
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QY	613	TC	AG	CGCGCGCCCCCGCCACACGCT	AGTGTGACCCCGAAGGCGT	TGGGATGCGAAGCGGC	672
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QY	601	TC	AG	CGCGCGCCCCCGCCACACGCT	AGTGTGACCCCGAAGGCGT	TGGGATGCGAAGCGGC	660
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QY	673	CT	TG	GAACATAGCTCAGGAGGCGG	GCTCCCCCTTGGGCTTCCCA	AGCCCGGTTGCGAG	732
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QY	661	CT	TG	GAACATAGCTCAGGAGGCGG	GCTCCCCCTTGGGCTTCCCA	AGCCCGGTTGCGAG	720
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QY	733	GAG	CG	CGGGGCGAGTGTCCAGCCGA	AGCTGTGCGCTTGC	CAAGAGGCCAGGCGTGGCG	792
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QY	721	GAG	CG	CGGGGCGAGTGTCCAGCCGA	AGCTGTGCGCTTGC	CAAGAGGCCAGGCGTGGCG	780
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QY	793	TG	CC	CCCTGAGCCGAGCGGACGCC	CGCTTGGGCGAGGCTCT	TGGGCCACCCCGGCGAGGAC	852
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QY	853	CG	TG	GACCGACCGAGTACCGTGGT	TCTGTGTGTGTGTACCT	TGCGACACCCCGCGAAGAAC	912
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QY	913	CAC	CT	CTTTGGAGGTGCGCTCTCTG	CGACGCGCACTCCAC	CCATCCCGTGGGCGCGCA	972
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QY	901	CAC	CT	CTTTGGAGGTGCGCTCTCTG	CGACGCGCACTCCAC	CCATCCCGTGGGCGCGCA	960
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QY	961	GC	AC	CGCGGGGCCCCCATCCATAT	CGCGGCCACCA	CGTCCCTTGGGACACGCTTGTCC	1020
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QY	1033	CC	GC	GCGGTGTACCGAGACCAAG	ACTTCTCTACTCTCTAGGG	CGCAAGGAGCAGTGTGG	1092
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QY	1093	GC	CT	CTCTCTACTAGCTCTCTG	AGGCCCGACGCTGAC	TGCGGCTCGGAGGCTCGTGA	1152
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QY	1081	GC	CT	CTCTCTACTAGCTCTCTG	AGGCCCGACGCTGAC	TGCGGCTCGGAGGCTCGTGA	1140
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Qy	1153	GACCATCTTCTTGGGTTCCAGGCCCTCGATGCGCAGAGGACTCCCGCAGGTTGCCCGCCCT	1212
Db	1141	GACCATCTTCTTGGGTTCCAGGCCCTCGATGCGCAGAGGACTCCCGCAGGTTGCCCGCCCT	1200
Qy	1213	GCCTCAGCGCTACTGGCAATCGGCCCTCTGTTCTCGAGCTGCTTGGGAACACACGGCA	1272
Db	1201	GCCTCAGCGCTACTGGCAATCGGCCCTCTGTTCTCGAGCTGCTTGGGAACACACGGCA	1360
Qy	1273	GTGCCCCATAGGGGTGCTCCTCAAGACGCACCTGCCGCTCGAGAGCTCGGTACACCCAGC	1332
Db	1261	GTGCCCCATAGGGGTGCTCCTCAAGACGCACCTGCCGCTCGAGAGCTCGGTACACCCAGC	1320
Qy	1333	AGCCGGTGTGTGTCGCCGGAGAAAGCCCAAGGCTCTGTGGCGGCCCGCCGAGAGAGGA	1392
Db	1321	AGCCGGTGTGTGTCGCCGGAGAAAGCCCAAGGCTCTGTGGCGGCCCGCCGAGAGAGGA	1380
Qy	1393	CACAGACCCCGCTCGCTGTGACGTGCTCCGACAGCACAGCAGACGCCCTGGCAGAGTGA	1452
Db	1381	CACAGACCCCGCTCGCTGTGACGTGCTCCGACAGCACAGCAGACGCCCTGGCAGAGTGA	1440
Qy	1453	CGGCTTCGTGCGGGCCTGCCCTGCGCCGCTGTGTGCCCCAGGCTCTGGGGCTCCAGGCA	1512
Db	1441	CGGCTTCGTGCGGGCCTGCCCTGCGCCGCTGTGTGCCCCAGGCTCTGGGGCTCCAGGCA	1500
Qy	1513	CAACGAACGCCGCTTCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGGAAGCATGCGAA	1572
Db	1501	CAACGAACGCCGCTTCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGGAAGCATGCGAA	1560
Qy	1573	GCTCTCGCTGCAGGAGCTGACGTGGAGATGAGCGTGGGAGCTGGCTTGGCTGGCGAG	1632
Db	1561	GCTCTCGCTGCAGGAGCTGACGTGGAGATGAGCGTGGGAGCTGGCTTGGCTGGCGAG	1620
Qy	1633	GAGCCACAGGGTGGCTGTGTTCCGGCCGCAGAGCACCGCTGCGTGGAGAGATCCTGGC	1692
Db	1621	GAGCCACAGGGTGGCTGTGTTCCGGCCGCAGAGCACCGCTGCGTGGAGAGATCCTGGC	1680
Qy	1693	CAAGTTCCTGCACPGCTGATGAGTGTACGTCGTGAGCTGCTCAGGTCCTTTCCTTTTA	1752
Db	1681	CAAGTTCCTGCACPGCTGATGAGTGTACGTCGTGAGCTGCTCAGGTCCTTTCCTTTTA	1740
Qy	1753	TGTCACGGAGACCAAGTTTCAAGACAGGCTCTTTTCTACGGAGAGTCTCTGGAG	1812
Db	1741	TGTCACGGAGACCAAGTTTCAAGACAGGCTCTTTTCTACGGAGAGTCTCTGGAG	1800
Qy	1813	CAAGTTCGAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTCGGGAGCTGTC	1872
Db	1801	CAAGTTCGAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTCGGGAGCTGTC	1860
Qy	1873	GGAAGCAGAGGTACAGCAGCATCGGGAAGCCAGCCCGCCCTGCTACGTCCTCAGACTCCG	1932
Db	1861	GGAAGCAGAGGTACAGCAGCATCGGGAAGCCAGCCCGCCCTGCTACGTCCTCAGACTCCG	1920
Qy	1933	CTTCATCCCAAGCCTACGGCTGCGGCCGATGTGAACATGGACTACGTCGCTGGAGC	1992
Db	1921	CTTCATCCCAAGCCTACGGCTGCGGCCGATGTGTGAACATGGACTACGTCGCTGGAGC	1980
Qy	1993	CAGAACTTCGCGAGAAAAAGAGGCCGAGCGCTCTCACCTCGAGGGTGAAGCACTGTT	2052
Db	1981	CAGAACTTCGCGAGAAAAAGAGGCCGAGCGCTCTCACCTCGAGGGTGAAGCACTGTT	2040
Qy	2053	CAGCGTCTCAACTACAGCGGGCGGGCCCGCCCGCCCTCTGTGGCGCCCTCTGTGTGGG	2112
Db	2041	CAGCGTCTCAACTACAGCGGGCGGGCCCGCCCGCCCTCTGTGTGGG	2100
Qy	2113	CCTGGACGATATCCACAGGGCCTGGCGCACCTTCTGTGCTGCTGGGCCCGAGNCCC	2172
Db	2101	CCTGGACGATATCCACAGGGCCTGGCGCACCTTCTGTGCTGCTGGGCCCGAGNCCC	2160
Qy	2173	GCSCCTGAGCTGTACTTCTCAAGTGTGATGTGACGGGCGCTGACACACCATCCCCCA	2232
Db	2161	GCSCCTGAGCTGTACTTCTCAAGTGTGATGTGACGGGCGCTGACACACCATCCCCCA	2220
Qy	2233	GGACAGGCTCACGGAGGTATCGCCAGCATCATCAACCCCGAGAACAGTACTGCTGGCG	2292

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QY 2293 TCGGTATGCGGTGTCAGAAAGCCGATGGGACAGCTCGGCAAGGCTTCAAGAGCCA 2352  
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QY 2353 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGATTGCTGGCTCACTCAGGA 2412  
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QY 2413 GACAGCCCGCTGAGGGATGCGGTGCTCATCGACAGAGCTCCTCCCTGAATGAGGCCAG 2472  
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Db 2821 GCGGCCCCAGCGCTTATCCCTGTGTGGGCTGCTGTGTGATACCCGACCCCTGGAGT 2880  
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QY 2893 CGAGAGCACTACTCCAGTATGCGCGGACCTCCATCAGAGCACTCAGCTTCAACCG 2952  
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QY 3073 CAAATCTCTGCTGAGGGGTACAGGTTTACCGCATGTGTGTCAGCTCCCATTTCA 3132  
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Db 3181 CTGCTACTCCATCTTGAAGAACCCAGGATGTGCTGGGGGCAAGGGCGCGCG 3240  
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QY 3253 CGGCGCTCTGCGCTCCGAGGCGGTGCAAGTGTGTGCCAACCAAGCATTTCTGCTCAAGT 3312  
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Db 3241 CGGCGCTCTGCGCTCCGAGGCGGTGCAAGTGTGTGCCAACCAAGCATTTCTGCTCAAGT 3300  
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Db 3301 GACTCGACACCGTGTCACTACCTAGTGCACACTCTCTGGGGTCACTCAGGACAGCCAGACGA 3360  
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QY 3433 ACTGCCCTCAGACTTCAAGACCATCTTGACTGTAGTGGCCACCCGCCACAGCCAGGCCGA 3492  
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTTGACTGTAGTGGCCACCCGCCACAGCCAGGCCGA 3480  
QY 3493 GAGCAGACACAGCAGCCCTGTACGCGGGGCTCTACGTCCAGGAGGAGGGGGCGCG 3552  
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QY 3553 CACACCCAGGCGCCGACCGCTGGAGTCTGAGGCTGAGTGTGTTGCGCGAGGCGCTG 3612  
Db 3541 CACACCCAGGCGCCGACCGCTGGAGTCTGAGGCTGAGTGTGTTGCGCGAGGCGCTG 3600  
QY 3613 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT 3672  
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QY 3673 GAGTCTCCAGCACACCTGCGCTTTCACTTCCCCACAGGCTGCGCTCGGCTCCACCCA 3732  
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QY 3733 GGGCAGCTTTTCCCTCACCAGGAGCGCGCTTCCACTCCCCACATAGGAATAGTCCATCC 3792  
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QY 3793 CCGTAT 3798  
Db 3781 CCAGAT 3786

RESULT 5

US-09-572-423B-3  
; Sequence 3, Application US/09572423B  
; Patent No. 6331399  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: William A. Gaarde  
; APPLICANT: Edward Wancewicz  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION  
; FILE REFERENCE: ISPH-0462  
; CURRENT APPLICATION NUMBER: US/09/572,423B  
; CURRENT FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 29  
; SEQ ID NO 3  
; LENGTH: 4015  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (56)...(3454)  
US-09-572-423B-3

Query Match 99.6%; Score 3784.4; DB 4; Length 4015;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 GCAGCGCTGCGTCTGCTGCGCACGTGGGAAGCCCTGGCCCGGCGCACCCCGCGATGCC 72  
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QY 73 GCGCGCTCCCGCTGCGGAGCGGTGGCTCCCTGCTGCGCAGCAGCTACCGGAGGTGT 132  
Db 61 GCGCGCTCCCGCTGCGGAGCGGTGGCTCCCTGCTGCGCAGCAGCTACCGGAGGTGT 120  
QY 133 GCGCGTGGCAGCTTGTGCGGCGGTGGGGCCCGCAGGCGTGGCGGCTGCGAGCGCG 192  
Db 121 GCGCGTGGCAGCTTGTGCGGCGGTGGGGCCCGCAGGCGTGGCGGCTGCGAGCGCG 180

QY	193	GGACCCGGCGGCTTTCGCGCGCTGTGTGGGCCAGTGTGCTGTGGTGTGCTGCCCTGGGACGC	255
Db	181	GGACCCGGCGGCTTTCGCGCGGCTGTGTGGGCCAGTGTGCTGTGGTGTGCTGCCCTGGGACGC	240
QY	253	ACGGCGCCCGCCGCGCGCCCTCTCTTCGCGCAGGTGTCTGCTGAAGAGCTGTGGC	312
Db	241	ACGGCGCCCGCCGCGCGCCCTCTCTTCGCGCAGGTGTCTGCTGAAGAGCTGTGGG	300
QY	313	CCGAGTGTCTGCAGAGGTGTGTGCGAGCGCGCGGAAGACTGTGTCGCTTTCGGCTTTCGC	372
Db	301	CCGAGTGTCTGCAGAGGTGTGTGCGAGCGCGCGGAAGACTGTGTCGCTTTCGGCTTTCGC	360
QY	373	GCTGCTGGACGGGGCCCGGGGGCCCTTACACACAGCTGTGCGCCTTACACACAGCTGTGCGCAGCTA	432
Db	361	GCTGCTGGACGGGGCCCGGGGGCCCTTACACACAGCTGTGCGCCTTACACACAGCTGTGCGCAGCTA	420
QY	433	CTGCCCCAACACAGGTGTACGACGACGTGCGGGGAGCGGGGCTGTGGGGCTGTGCTGCGG	492
Db	421	CTGCCCCAACACAGGTGTACGACGACGTGCGGGGAGCGGGGCTGTGGGGCTGTGCTGCGG	480
QY	493	CCGCGTGGGCGACAGCTGTGTGTTACCTGTCTGGCACGCTGCGCGCTCTTTGTGTGCTGGT	552
Db	481	CCGCGTGGGCGACAGCTGTGTGTTACCTGTCTGGCACGCTGCGCGCTCTTTGTGTGCTGGT	540
QY	553	GGCTCCAGTGTGCGCTTACACAGTGTGCGGGCGCGCGCTGTATACAGCTCGCGCGTGTGCAC	612
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QY	613	TCAGGCGCGCGCCCGCCACACGCTAGTGTGACCCCGAAGCGTGTGGATGTGCGAACCGGC	672
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QY	673	CTGGAACCATAGCTCAGGAGGCGGGGTCCCGCTTGGGCTGTCCAGCCCGGGTGTGCGAG	732
Db	661	CTGGAACCATAGCTCAGGAGGCGGGGTCCCGCTTGGGCTGTCCAGCCCGGGTGTGCGAG	720
QY	733	GAGGCGGGGGCAGTGTCCACGCACTGTGCGCTTGTCCCAAGAGGCCCAAGGCGTGTGCGC	792
Db	721	GAGGCGGGGGCAGTGTCCACGCACTGTGCGCTTGTCCCAAGAGGCCCAAGGCGTGTGCGC	780
QY	793	TGCCCTTAGCGGAGCGGACGCGCTGTGGCAGGGGTCTGGGCCACACCGGGCAGGAC	852
Db	781	TGCCCTTAGCGGAGCGGACGCGCTGTGGCAGGGGTCTGGGCCACACCGGGCAGGAC	840
QY	853	GCCTGGACCGAGTGACCGTGTCTGTGTGTGTCTACCTGCCAGACCCCGCCGAAGAAGC	912
Db	841	GCCTGGACCGAGTGACCGTGTCTGTGTGTGTCTACCTGCCAGACCCCGCCGAAGAAGC	900
QY	913	CACCTCTTTGGAGGTGGCTCTGTGCGACGGGCACTCCACCCATCTGCTGGGCGGCCCA	972
Db	901	CACCTCTTTGGAGGTGGCTCTGTGCGACGGGCACTCCACCCATCTGCTGGGCGGCCCA	960
QY	973	GCACACGGGGCCCCCATCATCGCGGCCACACGTCCTTGGGACACGCTTGTCTG	1032
Db	961	GCACACGGGGCCCCCATCATCGCGGCCACACGTCCTTGGGACACGCTTGTCTG	1020
QY	1033	CCCGGTGTACCGCGAGACCAAGCACTTCTCTACTCTCATGGGACAAAGAGAGCTGTGCG	1092
Db	1021	CCCGGTGTACCGCGAGACCAAGCACTTCTCTACTCTCATGGGACAAAGAGAGCTGTGCG	1080
QY	1093	GCGCTCTCTCTACTCATGCTCTGTAGGGCCCCAGCTGACTGTGGGCTCGGAGGCTGTGGA	1152
Db	1081	GCGCTCTCTCTACTCATGCTCTGTAGGGCCCCAGCTGACTGTGGGCTCGGAGGCTGTGGA	1140
QY	1153	GACCATCTTTCTGGGTTCAGGCCCTGGATGCCAGGGACTTCCCCGCAAGTGTGCCCGCCT	1212
Db	1141	GACCATCTTTCTGGGTTCAGGCCCTGGATGCCAGGGACTTCCCCGCAAGTGTGCCCGCCT	1200
QY	1213	GCCCCAGCGCTACTTGGCAAAATGCGGCCCTGTCTTGTGAGCTGCTTGGGAACCAACGCGCA	1272
Db	1201	GCCCCAGCGCTACTTGGCAAAATGCGGCCCTGTCTTGTGAGCTGCTTGGGAACCAACGCGCA	1260
QY	1273	GTGCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTACCCCCAGC	1332

1261	Db	 GTGCCCTACGGGGTGCTCTCAAGACGCACTGCGCGTGCAGTGTGGCTCACCCGAG	1320
1333	Qy	AGCCGGTGCTGTGCCCGGAGAACCCAGAGGCTCTGTGGCGGCCCGAGGAGAGGA	1392
1321	Db	AGCCGGTGCTGTGTGCCCGGAGAACCCAGAGGCTCTGTGGCGGCCCGAGGAGAGGA	1380
1393	Qy	CACAGACCCCGTGCCTTGGTGACGTGCTCGCCAGACACAGACAGCCCTGGCAGGTGA	1452
1381	Db	CACAGACCCCGTGCCTTGGTGACGTGCTCGCCAGACACAGACAGCCCTGGCAGGTGA	1440
1453	Qy	CGGCTTCGTGGGGGCTGCCTGCGCGGGTGCTGTGCCCGCAGGCGCTCTGGGGTCCAGGCA	1512
1441	Db	CGGCTTCGTGGGGGCTGCCTGCGCGGGTGCTGTGCCCGCAGGCGCTCTGGGGTCCAGGCA	1500
1513	Qy	CAACGAACCGCGCTTCCTCAGGAACACCAAGAAGTTCACTCCCTGGGGAACATGCCAA	1572
1501	Db	CAACGAACCGCGCTTCCTCAGGAACACCAAGAAGTTCACTCCCTGGGGAACATGCCAA	1560
1573	Qy	GCTCTGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGAGTGCCTTGGCTGCGCAG	1632
1561	Db	GCTCTGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGAGTGCCTTGGCTGCGCAG	1620
1633	Qy	GAGCCAGGGGTGGCTGTGTTCCGGCGCAGAGCACCGTCTGCTGAGAGATCTCTGGC	1692
1621	Db	GAGCCAGGGGTGGCTGTGTTCCGGCGCAGAGCACCGTCTGCTGAGAGATCTCTGGC	1680
1693	Qy	CAAGTCTCGACGTGGCTGATGAGTGTACGTGCTGAGAGTGCCTCAGGCTCTTCTTTTA	1752
1681	Db	CAAGTCTCGACGTGGCTGATGAGTGTACGTGCTGAGAGTGCCTCAGGCTCTTCTTTTA	1740
1753	Qy	TGTCACGGAGACCGTTCCTAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1812
1741	Db	TGTCACGGAGACCGTTCCTAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1800
1813	Qy	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGGAAGAGGGTGCACTGCGGGAGCTGTC	1872
1801	Db	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGGAAGAGGGTGCACTGCGGGAGCTGTC	1860
1873	Qy	GGAAGCAGAGTTCAGGCAGCATCGGAAGCCAGCGCCGCTGCTACCTCCAGACTCCG	1932
1861	Db	GGAAGCAGAGTTCAGGCAGCATCGGAAGCCAGCGCCGCTGCTACCTCCAGACTCCG	1920
1933	Qy	CTTCATCCCCAAGCCTGACGGGCTCGGGCCGATTGTGAACATGGACTAGCTCTGTGGGAGC	1992
1921	Db	CTTCATCCCCAAGCCTGACGGGCTCGGGCCGATTGTGAACATGGACTAGCTCTGTGGGAGC	1980
1993	Qy	CAGAACGTTCCGCAGAGAAAAGAGGGCGCAGCGCTCTACCTCAGGGGTGAAGCACTGTT	2052
1981	Db	CAGAACGTTCCGCAGAGAAAAGAGGGCGCAGCGCTCTACCTCAGGGGTGAAGCACTGTT	2040
2053	Qy	CAGCGTGTCAACTACGAGCGGGCGCGCCCGCCGCTCCTCGTGGCGCTCTGTGCTGGG	2112
2041	Db	CAGCGTGTCAACTACGAGCGGGCGCGCCCGCCGCTCCTCGTGGCGCTCTGTGCTGGG	2100
2113	Qy	CCTGGACGATATCCACAGGGGCTGGCGCACTTCGTGCTGCGTGTGGGGCCCGCAGGACCC	2172
2101	Db	CCTGGACGATATCCACAGGGGCTGGCGCACTTCGTGCTGCGTGTGGGGCCCGCAGGACCC	2160
2173	Qy	GCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGGTACGACACCATCCCCCA	2232
2161	Db	GCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGGTACGACACCATCCCCCA	2220
2233	Qy	GGACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGACACACTACTGCGTGGG	2292
2221	Db	GGACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGACACACTACTGCGTGGG	2280
2293	Qy	TCGGTATGCCGTGTCTCCAGAAGCGCGCCATGGGCACGTCGCGAAGGCCCTCTCAAGAGCCA	2352
2281	Db	TCGGTATGCCGTGTCTCCAGAAGCGCGCCATGGGCACGTCGCGAAGGCCCTCTCAAGAGCCA	2340
2353	Qy	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGTGGGTCACTGCAGGA	2412





QY 13 GCAGGCTCGCTCCTGCTGCGCACGTTGGGAAGCCCTGGCCCGCGGCACCCCGCGATGCC 72  
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QY 73 GCGCGCTCCCGCTGCGCGAGCGGTGCGTCTGCTGCGCAGCCACTACCGAGAGTGT 132  
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QY 133 GCGCGTGGCAGCTGCTGCGCGCGCTTGGGCGCCAGGCGTGGGCGTGGTGCAGCGGG 192  
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121 GCGCGTGGCAGCTGCTGCGCGCGCTTGGGCGCCAGGCGTGGGCGTGGTGCAGCGGG 180  
QY 193 GGACCCGCGGCTTCCCGCGCGCTGCTGCGCGAGTGCCTGCTGCTGCGTGGAGCG 252  
DB |||||  
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QY 253 ACGGCGCGCGCGCGCGCGCTTCCCTGCGCGAGTGTCTGCTGCGTGAAGAGTGTGGG 312  
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241 ACGGCGCGCGCGCGCGCGCTTCCCTGCGCGAGTGTCTGCTGCGTGAAGAGTGTGGG 300  
QY 313 CCGAGTGTGAGAGGCTGTCGAGCGCGCGCGAGGCTTCCACACAGCTGCGCAGCTA 432  
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301 CCGAGTGTGAGAGGCTGTCGAGCGCGCGCGAGGCTTCCACACAGCTGCGCAGCTA 420  
QY 373 GCTGCTGAGCGGCG 432  
DB |||||  
361 GCTGCTGAGCGGCG 420  
QY 433 CCG 492  
DB |||||  
421 CCG 480  
QY 493 CCGCGTGGCGCAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 552  
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481 CCGCGTGGCGCAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
QY 553 GGTCTCCAGCTGCGGCTTACCAGGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 612  
DB |||||  
541 GGTCTCCAGCTGCGGCTTACCAGGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 600  
QY 613 TCAGCG 672  
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QY 673 CTGGAACCATACGCTCAGGAGCGCGGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCG 732  
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841 GCGTGGACCGAGTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
QY 913 CACCTCTTTGGAGGTGCGCTCTTGGCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 972  
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QY 973 GCACACGCGGCG 1032  
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1141 GACCATCTTTCTGGGTTCCAGGCGCTGGATGCCAGGACTTCCCGCAGGTTGCCCGCGCT 1200  
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1201 GCCCAGCGCTACTGGCAATTCGCGCGCGCTTTCTGAGGCTGCTTGGGAACGACGCGCA 1260  
QY 1273 GTGCCCTTACGGGCTGCTCCTCAAGACGACTTCCCGCTGCGAGCTGCGGTCACCCAGC 1332  
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2221	Db	GG	CAGGCTCACGGAGGTCAATCGCCAGCATCATCAAAACCCAGAAACAGTACTCGGTGCG	2280
2293	Qy	TC	GGTATGCCGTGGTCCAGAAGCCGCCCATGGGCAGCTCCGCAAGGCCCTTCAAGAGCCA	2352
2281	Db	TC	GGTATGCCGTGGTCCAGAAGCCGCCCATGGGCAGCTCCGCAAGGCCCTTCAAGAGCCA	2340
2353	Qy	CG	TCTCTACTCTTGACAGACCTCCAGCGGTACATCGGACAGTTCTGTTGGCTCACTGCAGGA	2412
2341	Db	CG	TCTCTACTCTTGACAGACCTCCAGCGGTACATCGGACAGTTCTGTTGGCTCACTGCAGGA	2400
2413	Qy	GACC	AGCCCGCTGAGGGATCCGTCGTATCAGACAGAGCTCTCCCTGAATCAGGCCAG	2472
2401	Db	GACC	AGCCCGCTGAGGGATCCGTCGTATCAGACAGAGCTCTCTCTGAATGAGGCCAG	2460
2473	Qy	CAG	TGGCCTCTTCGACGTCCTTCTACGCTTCATGTGCCACACGCGCTGCGCATCAGGG	2532
2461	Db	CAG	TGGCCTCTTCGACGTCCTTCTACGCTTCATGTGCCACACGCGCTGCGCATCAGGG	2520
2533	Qy	CAG	TCTTACGTCAGGCCAGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG	2592
2521	Db	CAAG	TCTTACGTCAGGCCAGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG	2580
2593	Qy	CAG	CTGTGCTACGGCGACATGGAGAACAAAGCTGTTTGGGGGATTGGGGGACAGGGCT	2652
2581	Db	CAG	CTGTGCTACGGCGACATGGAGAACAAAGCTGTTTGGGGGATTGGGGGACAGGGCT	2640
2653	Qy	GC	TCTCGGTTTGGTGGATGATTTCTTTGTTGGTGACACCTCACCTCACCCACCGCAAAAC	2712
2641	Db	GC	TCTCGGTTTGGTGGATGATTTCTTTGTTGGTGACACCTCACCTCACCCACCGCAAAAC	2700
2713	Qy	CT	TCTCAGACACCTGGTCGAGGTGTCCCTGAGTATGCTGCTGGTGACCTTTCGAGAA	2772
2701	Db	CT	TCTCAGACACCTGGTCGAGGTGTCCCTGAGTATGCTGCTGGTGACCTTTCGAGAA	2760
2773	Qy	GAC	AGTGGTGAACCTTCCTCTAGAAGACGAGGCCCTGGGTGGCAGCGCTTTTCTTCAGAT	2832
2761	Db	GAC	AGTGGTGAACCTTCCTCTAGAAGACGAGGCCCTGGGTGGCAGCGCTTTTCTTCAGAT	2820
2833	Qy	GC	CGCCACCGGCTATTTCCCTTGGTGGCGCTGCTGCTGGATACCCGACCCCTGGAGT	2892
2821	Db	GC	CGCCACCGGCTATTTCCCTTGGTGGCGCTGCTGCTGGATACCCGACCCCTGGAGT	2880
2893	Qy	GC	AGCGACTACTCCAGCTATCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG	2952
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2953	Qy	CG	CTTCAAGGCTGGGAGAACATGGGTGCGAAACTCTTTGGGGCTTTCGGGTGAAGTG	3012
2941	Db	CG	CTTCAAGGCTGGGAGAACATGGGTGCGAAACTCTTTGGGGCTTTCGGGTGAAGTG	3000
3013	Qy	TC	ACAGCTGTTTCTGGATTTGCAAGTGAACGCCCTCCAGACGGTGTGACCAACAATCTA	3072
3001	Db	TC	ACAGCTGTTTCTGGATTTGCAAGTGAACGCCCTCCAGACGGTGTGACCAACAATCTA	3060
3073	Qy	CA	AGATCTCTGCTGCAGCGGTACAGGTTTACGCGATGTGTGCTGCAGCTCCCATTTCA	3132
3061	Db	CA	AGATCTCTGCTGCAGCGGTACAGGTTTACGCGATGTGTGCTGCAGCTCCCATTTCA	3120
3133	Qy	TC	AGAAAGTTGGAAGAACCCACATTTTCTTGGCGCTCATCTCTGACACGGCTTCCCT	3192
3121	Db	TC	AGAAAGTTGGAAGAACCCACATTTTCTTGGCGCTCATCTCTGACACGGCTTCCCT	3180
3193	Qy	CT	GCTACTCCATCCTGAAAGCCAAAGACGAGGGATGTCTGCTGGGGGCCAAGGGCGCCG	3252
3181	Db	CT	GCTACTCCATCCTGAAAGCCAAAGACGAGGGATGTCTGCTGGGGGCCAAGGGCGCCG	3240
3253	Qy	CG	CCCTCTGCCCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCAATTCCTGTCTCAAGCT	3312
3241	Db	CG	CCCTCTGCCCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCAATTCCTGTCTCAAGCT	3300

## RESULT 7

US-09-675-321-1

03 03 075 321 1  
; Sequence 1, Application US/09675321

; sequence 1, Applicant  
; Patent No. 6440735

; FACILITY NO. 0440735  
; GENERAL INFORMATION:

APPLICANT: Gaeta, Federico C.A.

APPLICANT: Geron Corporation

; TITLE OF INVENTION: Methods and Compositions for Elic

; TITLE OF INVENTION: Response to a Telome

; FILE REFERENCE: 015389-003500PC

; CURRENT APPLICATION NUMBER: US/09/675,3

; CURRENT FILING DATE: 2000-09

; PRIOR APPLICATION NUMBER: US 60/112,006

; PRIOR FILING DATE: 1998-03-31

; PRIOR APPLICATION NUMBER: W0  
:  
: PRIOR FILING DATE: 1998-03-

; PRIOR FILING DATE: 1999-03-  
: NUMBER OF SEQ ID NOS: 2

; NUMBER OF SEQ  
: SOFTWARE: Pat

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; SOFTWARE: PAT
. SEQ ID NO 1

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; SEQ ID NO 1
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; LENGTH: 4013
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TYPE: DNA  
ORGANISM:

ORGANISM: HOMO  
; FEATURE:

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; FEATURE.
; NAME/KEY: CDS

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; LOCATION: (56)..(3454)

LOCATION: ( )  
; OTHER INFORMATION:

### Query Match

Query Match 99.6%: Score 3784 4: DB 4: Length 4015:

Query Match 55.8%; Score 3784.4;  
Best Local Similarity 100.0%; Pred. No. 0;

Best local similarity 100.0%, FREQ. NO. 0;  
Matches 3785: Conservative 0: Mismatches 1: Indels 0: Gaps

[illegible]

Qy	73	CGCGCTCCCGCTGCGGAGCGGTGCGCTCCCTGCTGCGAGCCACTACCGGAGTGCCT	132
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Db	61	CGCGCTCCCGCTGCGGAGCGGTGCGCTCCCTGCTGCGAGCCACTACCGGAGTGCCT	120
Qy	133	CGCGCTGCGCACGTTCTGTCGGCGCTTGCGGCCCCCAGGGCTGCGGCTGTCAGACGCG	192
Db			
Db	121	CGCGCTGCGCACGTTCTGTCGGCGCTTGCGGCCCCCAGGGCTGCGGCTGTCAGACGCG	180
Qy	193	GGACCCGGCGGCTTTCCGCGCGCTGTCGGGCCCCAGTGCCTGCTGTCGTCGCCCTGAGGAGTGTGGC	252
Db			
Db	181	GGACCCGGCGGCTTTCCGCGCGCTGTCGGGCCCCAGTGCCTGCTGTCGTCGCCCTGAGGAGC	240
Qy	253	ACGGCGCCCGCGCGCGCCCTCTCTCCGCGAGGTGTCCTGCTGAAGAGTGTGGTGGC	312
Db			
Db	241	ACGGCGCCCGCGCGCGCCCTCTCTCTCCGCGAGGTGTCCTGCTGAAGAGTGTGGTGGC	300
Qy	313	CCGAGTCTGCAGAGGCTGTGCAGCGCGCGCGAAGAACGTGCTGGCCCTTCGGCTTCGC	372
Db			
Db	301	CCGAGTCTGCAGAGGCTGTGCAGCGCGCGCGAAGAACGTGCTGGCCCTTCGGCTTCGC	360
Qy	373	GCTGCTGGACGGGCGCGCGGGGCCCCCGGAGGCTTCACCAACAGCTGGCGCTGGCAGCTA	432
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Db	361	GCTGCTGGACGGGCGCGCGGGGCCCCCGGAGGCTTCACCAACAGCTGGCGCTGGCAGCTA	420
Qy	433	CTGTGCCAACACGGTGACCGACGGACTGCGGGGGAGCGGGGGTGTGTCGTGCG	492
Db			
Db	421	CCTGTCCCAACACGGTGACCGACGGACTGCGGGGGAGCGGGGGTGTGTCGTGCG	480
Qy	493	CCGGTGGGCGACGCTGCTGTTCACCTGCTGGACGCTGGCGCTTCCTTCGTGCTGGT	552
Db			
Db	481	CCGGTGGGCGACGCTGCTGTTCACCTGCTGGACGCTGGCGCTTCCTTCGTGCTGGT	540
Qy	553	GGCTCCAGCTGGGCTTACCAGTGTGCGGGCGCGCTGTACACAGCTCGGCGTGCAC	612
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Db	541	GGCTCCAGCTGGGCTTACCAGTGTGCGGGCGCGCTGTACACAGCTCGGCGTGCAC	600
Qy	613	TCAGGCCGCGCGCGCCACACGCTAGTGACCCCGAAGCGCTGTGGATGCGAAGCGG	672
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Db	601	TCAGGCCGCGCGCGCCACACGCTAGTGACCCCGAAGCGCTGTGGATGCGAAGCGG	660
Qy	673	CTGGAACATAGGTCAGGAGCGCGGGTCCCGCTGGGCTGCCAGCCCGGGTGCAG	732
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Qy	733	GAGCGCGGGGAGTGCCACGCGAAGTCTGCGCTTGCCCAAGAGGCCACAGGCGTGC	792
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Qy	793	TGCGCTGACCGGAGCGGACGCGGTGTCGGGAGGGTCTCTGGGCCACCCGGCGAGGAC	852
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Db	781	TGCGCTGACCGGAGCGGACGCGGTGTCGGGAGGGTCTCTGGGCCACCCGGCGAGGAC	840
Qy	853	GCCTGACCGAGTGACCGTGTCTGTCGTGTGTCTACCTGCCAGACCCCGCGAAGAC	912
Db			
Db	841	GCCTGACCGAGTGACCGTGTGTCTGTCGTGTGTCTACCTGCCAGACCCCGCGAAGAC	900
Qy	913	CACCTCTTTGGAGGGTGGCTCTCTGTCACGCGGCGACTCCACCATCTGGCGCGCA	972
Db			
Db	901	CACCTCTTTGGAGGGTGGCTCTCTGTCACGCGGCGACTCCACCATCTGGCGCGCA	960
Qy	973	GCACACGCGGGCCCCCATCCACATCGCGGCCACCACTCCCTGGGACACGCTTGTTC	1032
Db			
Db	961	GCACACGCGGGCCCCCATCCACATCGCGGCCACCACTCCCTGGGACACGCTTGTTC	1020
Qy	1033	CCCGGTGTACCGGAGACCAAGCACTTCTCTACTCTAGGGGACAAGGAGCAGCTGCG	1092
Db			
Db	1021	CCCGGTGTACCGGAGACCAAGCACTTCTCTACTCTCAAGGACCAAGGAGCAGCTGCG	1080
Qy	1093	GCCCTCCTCTACTCAGCTCTGTGAGGCCCGAGCTGACTGCGGCTCGGAGGCTCTGGA	1152
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Db 2461 CAGTGGCTCTTCGAGCTCTTCTAGCTTTCATGTGCCACACGCGGTGGCATCAGGGG 2520  
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Db 2641 GCTCTCGCTTTGGTGGATGATTTCTTGTGTGACACCTCACCTCACCCACCGGAAAC 2700  
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## RESULT 8

US-09-052-919-1  
; Sequence 1, Application US/09052919  
; Patent No. 644650  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin B.  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Antisense Compositions for Detecting and  
; TITLE OF INVENTION: Inhibiting Telomerase Reverse Transcriptase  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/052,919  
; FILING DATE: 31-MAR-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/974,549  
FILING DATE: 19-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/974,584  
FILING DATE: 19-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Parent, Annette S.  
REGISTRATION NUMBER: 42,058  
REFERENCE/DOCKET NUMBER: 015389-003600US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4015 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 56..3454  
OTHER INFORMATION: /product= "human telomerase reverse  
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US-09-052-919-1

Query Match 99.6%; Score 3784.4; DB 4; Length 4015;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB	121	GGCGGTGGCCAGGTTCGTGGCGGCTGGGGCCCGAGGCTGGGGCTGGTCAGCGCGG	180
QY	193	GGACCCGGCGGCTTCCCGCGCTGGTGCGCCAGTGCCTGTGTCGTCGCTGGAGCGC	252
DB	181	GGACCCGGCGGCTTTCGCGCGCTGGTGCGCCAGTGCCTGTGTCGTCGCTGGAGCGC	240
QY	253	ACGGCGCGCCCGCGCCCTCCCTCCGCGAGGTTCCTGCTGCGAGGAGCTGGTGGC	312
DB	241	ACGGCGCGCCCGCGCCCTCCCTCCGCGAGGTTCCTCCGCGAGGAGCTGGTGGC	300

QY	313	CCGAGTGTGACAGGCTGTGGAGCGCGGCGGAGAACGTGCTGGCTTCGGCTTGGC	372
DB	301	CCGAGTGTGACAGGCTGTGGAGCGCGGCGGAGAACGTGCTGGCTTCGGCTTGGC	360
QY	373	GCTGTGACGGGGCGGCGGCGGCGGCGGAGGCTTACACACAGCGTGGCGAGCTA	432
DB	361	GCTGTGACGGGGCGGCGGCGGCGGAGGCTTACACACAGCGTGGCGAGCTA	420
QY	433	CCTGCCCAACACGCTGACGACGACTGCGGGGGAGCGGGGCTGGGGGCTGCTGCTGG	492
DB	421	CCTGCCCAACACGCTGACGACGACTGCGGGGGAGCGGGGCTGGGGGCTGCTGCTGG	480
QY	493	CGCGTGGCGGACGACGCTGCTGGTTCACCTGCTGACGCTGCGGCGCTTGTGCTGGT	552
DB	481	CGCGTGGCGGACGACGCTGCTGGTTCACCTGCTGACGCTGCGGCGCTTGTGCTGGT	540
QY	553	GGCTCCAGCTGCGCTACACAGGTGTGGGGGCGCGCTGTACACAGCTGCGGCGTGGCAC	612
DB	541	GGCTCCAGCTGCGCTACACAGGTGTGGGGGCGCGCTGTACACAGCTGCGGCGTGGCAC	600
QY	613	TCAGGCGCGGCGGCGGCGGCGGCTAGTGGAGCCCGAAGGCGTCTGGGATGGAAGGCG	672
DB	601	TCAGGCGCGGCGGCGGCGGCGGCTAGTGGAGCCCGAAGGCGTCTGGGATGGAAGGCG	660
QY	673	CTGGAACCATAGCTCAGGAGGCGGGTCCCGCTGGGCTGCCAGCCCGGGTGGGAG	732
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QY	793	TGCCCCCTGAGCGGAGCGCGCGCTTGGGAGGGGCTCTGGGCGCCACCCGGGCGAGAC	852
DB	781	TGCCCCCTGAGCGGAGCGCGCGCTTGGGAGGGGCTCTGGGCGCCACCCGGGCGAGAC	840
QY	853	CGGTGGACGAGTACCGTGGTTCCTGTGTGTGTGTCACCTGCCACACCGCGGAGAACG	912
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QY	1093	GCCCTCTCTCTACTCAGCTCTCTCAGGCGGCGGCTGCTGCGGCTCGGAGGCTCGTGA	1152
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DB	1141	GACCATCTTCTGGGTTCCAGGCGCTGGATGCCAGGAGTCCCGCGAGGCTTCCCGCGCT	1200
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DB	1201	GCCCCAGGCTACTGGCAATGCGGCGGCTTTCTGGAGCTGCTTGGGAAACACCGGCA	1260
QY	1273	GTGCCCTTACGGGCTCTCTCAAGACGACCTGCGCGCTGCGAGTGGGCTCACCCGAGC	1332
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## RESULT 9

US-08-912-951-1  
; Sequence 1, Application US/08912951  
; Patent No. 6475789  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND  
; THERAPEUTIC METHODS  
; NUMBER OF SEQUENCES: 335  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912.951  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-0026000US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4015 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 56..3454  
; OTHER INFORMATION: /product= "hTERT"  
; OTHER INFORMATION: /note= "human telomerase reverse  
; transcriptase (hTERT) catalytic protein  
; OTHER INFORMATION: component"  
; US-08-912-951-1  
  
Query Match 99.6%; Score 3784.4; DB 4; Length 4015;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 13 GCAGCGCTGCGTCTGCTGCGCACGCTGGGAAGCCCTGGCCCGGCCACCCCGCGATGCC 72  
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Db 241 ACGGCG 300  
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1993	QY	CAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACTCTGAGGGTGAAGGACGTGTT	2052
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2053	QY	CAGCGTCTCAACTACGAGCGGGCGCGGCCCGCCCTCTGGGCGCCTCTGTGCTGGG	2112
2041	DB	CAGCGTCTCAACTACGAGCGGGCGCGGCCCGCCCTCTGGGCGCCTCTGTGCTGGG	2100
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2173	QY	GCGCCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGGCGGTACGACACCAATCCOCCCA	2232
2161	DB	GCGCCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGGCGGTACGACACCAATCCOCCCA	2220
2233	QY	GGACAGCTCAGGAGGTCTATCGCCAGCATCATCAAAACCCAGACAGCTACTTCGCTGGC	2292
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2401	DB	GACCAGCCCGCTGAGGGATCCGCTGTCATGCGACAGCTCTCTCCCTGATGAGGCCAG	2460
2473	QY	CAGTGGCCTCTTCGACCTCTTCTACGCTTTCATGTGCCACACGCCCTGCGCATCAGGGG	2532
2461	DB	CAGTGGCCTCTTCGACCTCTTCTACGCTTTCATGTGCCACACGCCCTGCGCATCAGGGG	2520
2533	QY	CAAGTCTCTAGTCCAGTGCACAGGGATCCCGCAGGGTCCCATCTCTCCACGTGCTGCTG	2592
2521	DB	CAAGTCTCTAGTCCAGTGCACAGGGATCCCGCAGGGTCCCATCTCTCCACGTGCTGCTG	2580
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2581	DB	CAGCCTGTGCTACGGGCACATGGAGAACAGCTGTTTTCGGGGGATTTCGGCGGGACGGGCT	2640
2653	QY	GCCTCTCGCTTTGGTGGATGATTTCTTTGTTGGTGACACCTCACCTCACCCACGCGAAAC	2712
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Qy	2953	CGGCTTCAAGGCTGGGAGGAACATGCGTGC	AAACTCTTTTGGGGTCTTGGCGTGAAGTG	3012
Db	2941	CGGCTTCAAGGCTGGGAGGAACATGCGTGC	AAACTCTTTTGGGGTCTTGGCGTGAAGTG	3000
Qy	3013	TCACAGCCTCTTCTGTGATTTGACAGGTGA	ACAGCCTCCACAGCGTGTGCACCAACATCTA	3072
Db	3001	TCACAGCCTCTTCTGTGATTTGACAGGTGA	ACAGCCTCCACAGCGTGTGCACCAACATCTA	3060
Qy	3073	CAAGATCCTCCTGCTGCAGCGGTACAGTTTC	ACAGCTGTGTGTCGAGCTCCCATTTTCA	3132
Db	3061	CAAGATCCTCCTGCTGCAGCGGTACAGTTTC	ACAGCTGTGTGTCGAGCTCCCATTTTCA	3120
Qy	3133	TCAGCAAGTTTGGAAAGAACCCACATTTTTC	TTCGTGGCGTCACTCTGTACAGGGCTCCCT	3192
Db	3121	TCAGCAAGTTTGGAAAGAACCCACATTTTTC	TTCGTGGCGTCACTCTGTACAGGGCTCCCT	3180
Qy	3193	CTGCTACTCCTACTCTGAAAGCAAGACGAG	CGGATGTCTGCTGGGGCCAAAGGCGCGC	3252
Db	3181	CTGCTACTCCTACTCTGAAAGCAAGACGAG	CGGATGTCTGCTGGGGCCAAAGGCGCGC	3240
Qy	3253	CGGCGCTCTGCCCTCGAGGCGGTGCA	TGTGGCTGTGCCACCAAGCATTCCTGTCAAGCT	3312
Db	3241	CGGCGCTCTGCCCTCGAGGCGGTGCA	TGTGGCTGTGCCACCAAGCATTCCTGTCAAGCT	3300
Qy	3313	GACTCGACACCGTGTCACTACCTGTC	GCACCTCTGGGTCACTCAGGACGCCCAGAGCA	3372
Db	3301	GACTCGACACCGTGTCACTACCTGTC	GCACCTCTGGGTCACTCAGGACGCCCAGAGCA	3360
Qy	3373	GCTGAGTGGGAAGCTCCCGGGAGCAG	CGCTGACTTGGCCCTGGAGGCGCAGCCAACCGGC	3432
Db	3361	GCTGAGTGGGAAGCTCCCGGGAGCAG	CGCTGACTTGGCCCTGGAGGCGCAGCCAACCGGC	3420
Qy	3433	ACTGCCCTCAGACTTCAGACCATCTGT	GACTGTGACCCAGCGCCACAGCCGCGA	3492
Db	3421	ACTGCCCTCAGACTTCAGACCATCTGT	GACTGTGACCCAGCGCCACAGCCGCGA	3480
Qy	3493	GAGCAGACACAGCAGCCCTGTACGCG	CGGGCTCTACGTCCAGGAGGAGGGGCGGC	3552
Db	3481	GAGCAGACACAGCAGCCCTGTACGCG	CGGGCTCTACGTCCAGGAGGAGGGGCGGC	3540
Qy	3553	CACACCCAGCCGCGCACCCTGGAGTCT	CAGGCGTGTAGTGTGGCCAGAGCGCTG	3612
Db	3541	CACACCCAGCCGCGCACCCTGGAGTCT	CAGGCGTGTAGTGTGGCCAGAGCGCTG	3600
Qy	3613	CATGTCCGGCTGAAGGCTGAGTGTCCG	GGCTTGAGGCTTGAGCGCTTCCAGCCAAAGGCT	3672
Db	3601	CATGTCCGGCTGAAGGCTGAGTGTCCG	GGCTTGAGGCTTGAGCGCTTCCAGCCAAAGGCT	3660
Qy	3673	GAGTGTCCAGCACACCTGTCCGTCTT	CACTTCCCCACAGGCTGGCGTTCGAGCTCCACGCCA	3732
Db	3661	GAGTGTCCAGCACACCTGTCCGTCTT	CACTTCCCCACAGGCTGGCGTTCGAGCTCCACGCCA	3720
Qy	3733	GGCCAGCTTTTCTCTACACAGGACCG	GGCTTCCACTTCCCCACATAGGAATAGTCCATCC	3792
Db	3721	GGCCAGCTTTTCTCTACACAGGACCG	GGCTTCCACTTCCCCACATAGGAATAGTCCATCC	3780
Qy	3793	CCTGAT	3798	
Db	3781	CCAGAT	3786	

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RESULT 10
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; Sequence 3, Application US/09733294A
; Patent No. 6492171
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODUL
; FILE REFERENCE: ISPH-0527

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; CURRENT APPLICATION NUMBER: US/09/733,294A
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; CURRENT FILING DATE: 2000-12-07
;
; PRIOR APPLICATION NUMBER: 09/572,423
;
; PRIOR FILING DATE: 2000-05-16
;
; NUMBER OF SEQ ID NOS: 108
;
; SEQ ID NO 3
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; LENGTH: 4015
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; TYPE: DNA
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; ORGANISM: Homo sapiens
;
; FEATURE:
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; NAME/KEY: CDS
;
; LOCATION: (56)...(3454)
US-09-733-294A-3

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Query Match		99.6%	Score 3784.4	DB 4	Length 4015
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QY	133	GCAGCGTGGCCACGTTCGTGCGGGCGCTGGGGCCCCAGGGCTGCGGCTGTCAGCGCGG	192		
DB	121	GCAGCGTGGCCACGTTCGTGCGGGCGCTGGGGCCCCAGGGCTGCGGCTGTCAGCGCGG	180		
QY	193	GGACCCCGCGGCTTTCCGCGCGCTGTGTGGGCCCACTGCTGTGTGCTGCCCTGGGACGC	252		
DB	181	GGACCCCGCGGCTTTCCGCGCGCTGTGTGGGCCCACTGCTGTGTGCTGCCCTGGGACGC	240		
QY	253	ACGGCGCGCCCGCGCGCCCTCCTTCGCGCCAGGTGCTCTGCTGAGGAGCTGGTGGC	312		
DB	241	ACGGCGCGCCCGCGCGCCCTCCTTCGCGCCAGGTGCTCTGCTGAGGAGCTGGTGGC	300		
QY	313	CCGAGTCTGCAGAGGCTGTGCGAGCGCGCGGAAGACGTGTGCGCCTTCGCGCTTCGC	372		
DB	301	CCGAGTCTGCAGAGGCTGTGCGAGCGCGCGGAAGACGTGTGCGCCTTCGCGCTTCGC	360		
QY	373	GCTGCTGGACGGGGCGCGGGGGCCCCCGGAGGCCCTTACACACAGCGTGGCAGCTA	432		
DB	361	GCTGCTGGACGGGGCGCGGGGGCCCCCGGAGGCCCTTACACACAGCGTGGCAGCTA	420		
QY	433	CCTGCCCAACACGCTGACCGACGACATGCGGGGGAGGGCGCTGCGGCGTGTGCTGCG	492		
DB	421	CCTGCCCAACACGCTGACCGACGACATGCGGGGGAGGGCGCTGCGGCGTGTGCTGCG	480		
QY	493	CCGCGTGGGCGACGACGTGTGTTACCTGTCTGGCACGCTGGCGCGCTCTTTGTGCTGT	552		
DB	481	CCGCGTGGGCGACGACGTGTGTTACCTGTCTGGCACGCTGGCGCGCTCTTTGTGCTGT	540		
QY	553	GGCTCCAGCTGGCGCTTACCAGTGTGCGGGCGCGCGCTGTACACGCTCGCGCTGCCAC	612		
DB	541	GGCTCCAGCTGGCGCTTACCAGTGTGCGGGCGCGCGCTGTACACGCTCGCGCTGCCAC	600		
QY	613	TCAGGCCCGCCCCCGCCACACGCTAGTGGACCCCGAAGCGCTGTGGGATGCGAACGGGC	672		
DB	601	TCAGGCCCGCCCCCGCCACACGCTAGTGGACCCCGAAGCGCTGTGGGATGCGAACGGGC	660		
QY	673	CTGGAACCATAGGCTCAGGAGGCGGGGTCCCCCTGGGCGCTGCCAGCCCCGGGTGGCAG	732		
DB	661	CTGGAACCATAGGCTCAGGAGGCGGGGTCCCCCTGGGCGCTGCCAGCCCCGGGTGGCAG	720		
QY	733	GAGCGCGGGGGGAGTGCCACGCGCAAGTCTGCGGTTGCCCAAGAGGCCCAAGGGCTGGCGC	792		
DB	721	GAGCGCGGGGGGAGTGCCACGCGCAAGTCTGCGGTTGCCCAAGAGGCCCAAGGGCTGGCGC	780		
QY	793	TGCCCTTGACCGAGCGGACGCCCGCTTGGGCAAGGGTCTCTGGGCCACACCCGGGCAAGAC	852		
DB	781	TGCCCTTGACCGAGCGGACGCCCGCTTGGGCAAGGGTCTCTGGGCCACACCCGGGCAAGAC	840		

QY	853	GGTGTGACCGAGTGACCGTGGTTTCTGTGTGGTGTACCTGCGAGACCGCGCGAAGAAGC	912	1933	CTTTCATCCCAAGCCTGACGGGTGCGCGGATGTGTGAACATGAGTACGTGCTGGGAGC	1992
Db	841	GGTGTGACCGAGTGACCGTGGTTTCTGTGTGGTGTACCTGCGAGACCGCGCGAAGAAGC	900	1921	CTTTCATCCCAAGCCTGACGGGTGCGCGGATGTGTGAACATGAGTACGTGCTGGGAGC	1980
QY	913	CACCTCTTTTGGAGGTGGCTCTCTGGCACGGCCACTCCACCCATCCGTGGCGCGCA	972	1993	CAGAAAGTTCCGCAGAGAAAAGAGGCCAGCGTCTCACTCGAGGGTGAAGCACTGTT	2052
Db	901	CACCTCTTTTGGAGGTGGCTCTCTGGCACGGCCACTCCACCCATCCGTGGCGCGCA	960	1981	CAGAAAGTTCCGCAGAGAAAAGAGGCCAGCGTCTCACTCGAGGGTGAAGCACTGTT	2040
QY	973	GCACCACGGGGCCCCCATCCACATCGCGGCCACACACTGCCTGGGACACGCTTGTGCC	1032	2053	CAGCGTGTCTCAACTACGACGGCGCGCGCCCGCCCTCCCTGGGGCGCTCTGTGTCTGG	2112
Db	961	GCACCACGGGGCCCCCATCCACATCGCGGCCACACACTGCCTGGGACACGCTTGTGCC	1020	2041	CAGCGTGTCTCAACTACGACGGCGCGCGCCCGCCCTCCCTGGGGCGCTCTGTGTCTGG	2100
QY	1033	CCGGGTGTAGCCGGAGACCAAGCACTTCTCTACTCTCTCAGCGCAACAGGACAGTGGG	1092	2113	CCTGGACGATATCCACAGGGCCCTGGCGCACCTTCGTCTGCTGCTGCGGCCCGCAGACCC	2172
Db	1021	CCGGGTGTAGCCGGAGACCAAGCACTTCTCTACTCTCTCAGCGCAACAGGACAGTGGG	1080	2101	CCTGGACGATATCCACAGGGCCCTGGCGCACCTTCGTCTGCTGCTGCGGCCCGCAGACCC	2160
QY	1093	GCCTCTCTTCTACTCAGCTCTCTGAGGCCACGCTGACTGCGCTCGGAGGCTCGTGGA	1152	2173	GGCGCTGTAGCTGTACTTTGTCAAGTGGATGTGACGGCGGGGTAGCACACCATCCCCCA	2232
Db	1081	GCCTCTCTTCTACTCAGCTCTCTGAGGCCACGCTGACTGCGCTCGGAGGCTCGTGGA	1140	2161	GGCGCTGTAGCTGTACTTTGTCAAGTGGATGTGACGGCGGGGTAGCACACCATCCCCCA	2220
QY	1153	GACCAFTCTTCTGGGTTCAGGCCCTTGGATGCCAGGGACTCCCGCAGGTTGCCCGCCT	1212	2233	GGACAGGCTCAGGGAGTTCATGCCACGATCATCAAAACCCCAAGAACCTTACTTGCCTGG	2292
Db	1141	GACCAFTCTTCTGGGTTCAGGCCCTTGGATGCCAGGGACTCCCGCAGGTTGCCCGCCT	1200	2221	GGACAGGCTCAGGGAGTTCATGCCACGATCATCAAAACCCCAAGAACCTTACTTGCCTGG	2280
QY	1213	GGCCAGCGCTACTGGCAATGCGGCCCTGTCTTCTGGAGCTGCTTGGGAACACGCGCA	1272	2293	TCGGTATGCCGTGTGCCAAGGCCCGCCCATGGGCACGTCCGCAAGGCCCTTCAAGAGCCA	2352
Db	1201	GGCCAGCGCTACTGGCAATGCGGCCCTGTCTTCTGGAGCTGCTTGGGAACACGCGCA	1260	2281	TCGGTATGCCGTGTGCCAAGGCCCGCCCATGGGCACGTCCGCAAGGCCCTTCAAGAGCCA	2340
QY	1273	GTGCCCTTCTAGGGTCTCCTCAAGACGACTTCCCGCTGCGAGCTGCGGTCACCCAGC	1332	2353	CGTCTCTACTCTGACAGACTCCAGCCGTACATGCGACAGTTCGTTGGCTTCCAGAGCCA	2412
Db	1261	GTGCCCTTCTAGGGTCTCCTCAAGACGACTTCCCGCTGCGAGCTGCGGTCACCCAGC	1320	2341	CGTCTCTACTCTGACAGACTCCAGCCGTACATGCGACAGTTCGTTGGCTTCCAGAGCCA	2400
QY	1333	AGCCGCTGTCTGTGCCGGGAGAACCCAGGGCTCTGTGGGGCCCCCGAGGAGGGA	1392	2413	GACCAAGCCGCTGAGGGATGCCGTCTCATCGAGCAGAGCTCCTCCTGAATGAGGCCAG	2472
Db	1321	AGCCGCTGTCTGTGCCGGGAGAACCCAGGGCTCTGTGGGGCCCCCGAGGAGGGA	1380	2401	GACCAAGCCGCTGAGGGATGCCGTCTCATCGAGCAGAGCTCCTCCTGAATGAGGCCAG	2460
QY	1393	CACAGACCCCGTGGCTGGTGTCTCCGACAGCACAGAGCCCTGGCAGGTGTA	1452	2473	CAGTGGCCCTTCGAGAGTCTTCTTACGCTTCACTGTGCCACACGCGCTGGCATCAGGG	2532
Db	1381	CACAGACCCCGTGGCTGGTGTCTCCGACAGCACAGAGCCCTGGCAGGTGTA	1440	2461	CAGTGGCCCTTCGAGAGTCTTCTTACGCTTCACTGTGCCACACGCGCTGGCATCAGGG	2520
QY	1453	CGGCTCTGTGGGGCTGCTGCGCGGCTGTGCCCGAGGCTCTTGGGGCTCCAGGCA	1512	2533	CAAGTCTACGCTCCAGGATCCGAGGGATCCCGAGGGCTCCATCCTTCCACGCTGCTCTG	2592
Db	1441	CGGCTCTGTGGGGCTGCTGCGCGGCTGTGCCCGAGGCTCTTGGGGCTCCAGGCA	1500	2521	CAAGTCTACGCTCCAGGATCCCGAGGGATCCCGAGGGCTCCATCCTTCCACGCTGCTCTG	2580
QY	1513	CAACGAACCCGCTTCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGGAAGCATGCCAA	1572	2593	CAGCCTGTGCTACGGCGACATGGAGAACAAAGTGTGTTGGGGGATTCGGCGGACCGGCT	2652
Db	1501	CAACGAACCCGCTTCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGGAAGCATGCCAA	1560	2581	CAGCCTGTGCTACGGCGACATGGAGAACAAAGTGTGTTGGGGGATTCGGCGGACCGGCT	2640
QY	1573	GCTCTGCTGCAGGAGCTGACGTGGNAGATGAGCGTGGGGACTGGCTTGGCTGGCGAG	1632	2653	GCTCTGCTGCTTGGTGGATGATTTCTTGTGTTGGTGACACCTCAGCTCACCACGCGGAAAC	2712
Db	1561	GCTCTGCTGCAGGAGCTGACGTGGNAGATGAGCGTGGGGACTGGCTTGGCTGGCGAG	1620	2641	GCTCTGCTGCTTGGTGGATGATTTCTTGTGTTGGTGACACCTCAGCTCACCACGCGGAAAC	2700
QY	1633	GAGCCAGGGTGGCTGTCTCCGGCCGACAGCACCGTCTGCGTGGAGAGATCCTGGC	1692	2713	CTTCTCTCAGACCTTGGTCCGAGGTGCTCCCTGAGTATGCTGCTGCTGCTGCTGCTGCTG	2772
Db	1621	GAGCCAGGGTGGCTGTCTCCGGCCGACAGCACCGTCTGCGTGGAGAGATCCTGGC	1680	2701	CTTCTCTCAGACCTTGGTCCGAGGTGCTCCCTGAGTATGCTGCTGCTGCTGCTGCTGCTG	2760
QY	1693	CAAGTCTCTGCACTGGCTGATCAGTGTGTAACGTCTGCTGCGAGCTCTTCTTTTA	1752	2773	GACAGTGTGTAACCTTCCCTGTAGAAGACAGGCCCTTGGGTGGCACCGCTTTTGTTCAGAT	2832
Db	1681	CAAGTCTCTGCACTGGCTGATCAGTGTGTAACGTCTGCTGCGAGCTCTTCTTTTA	1740	2761	GACAGTGTGTAACCTTCCCTGTAGAAGACAGGCCCTTGGGTGGCACCGCTTTTGTTCAGAT	2820
QY	1753	TGTCAGGAGACACGTTTCAAAAGAACAGAGTCTTTTCTACCGGAAGAGTGTCTGGAG	1812	2833	GGCGGCCACGAGGCTATTCCTCTGGTGGCGCTGCTGCTGGATACCCGAGCCCTTGAGGT	2892
Db	1741	TGTCAGGAGACACGTTTCAAAAGAACAGAGTCTTTTCTACCGGAAGAGTGTCTGGAG	1800	2821	GGCGGCCACGAGGCTATTCCTCTGGTGGCGCTGCTGCTGGATACCCGAGCCCTTGAGGT	2880
QY	1813	CAAGTGTCAAGCATTTGGAATCAGACAGCATTGAGAGGGTGCAGCTCGGGAGCTGTC	1872	2893	GCAGACGCACTACTCCAGCTATGCCGAGCTCCATCAGAGCCAGTCTCACCTTCAACCG	2952
Db	1801	CAAGTGTCAAGCATTTGGAATCAGACAGCATTGAGAGGGTGCAGCTCGGGAGCTGTC	1860	2881	GCAGAGCGACTACTCCAGCTATGCCGAGCTCCATCAGAGCCAGTCTCACCTTCAACCG	2940
QY	1873	GGAAGCAGAGGTGAGGACATCGGGAAGCCAGGCCCGCTGCTGACGCTCCAGACTCGG	1932	2953	CGGCTTCAAGGGTGGGAGGAACATGCGTCGCAAACTCTTTTGGGTCTTTCGGCTGAAGTG	3012
Db	1861	GGAAGCAGAGGTGAGGACATCGGGAAGCCAGGCCCGCTGCTGACGCTCCAGACTCGG	1920	2941	CGGCTTCAAGGGTGGGAGGAACATGCGTCGCAAACTCTTTTGGGTCTTTCGGCTGAAGTG	3000
				3013	TCACAGCCTGTTTCTGGATTTGCAAGTGAACAGCCTCCAGAGGGTGTGACCAACATCTA	3072



Db	61	CGCGCTCCCCGCTGCCGAGCCGTGCGTCCCTGCTGGCAGCCACTACCGCGAGGTGCT	120
Qy	133	CGCGCTGGCCACATGTTCTGTGGCGCGCTTGGGGCCCCAGGGCTTGGCGCTGTGTCAAGCGCGG	192
Db	121	CGCGCTGGCCACATGTTCTGTGGCGCGCTTGGGGCCCCAGGGCTTGGCGCTGTGTCAAGCGCGG	180
Qy	193	GGACCCGGCGGCTTTCCGGCGGCTTGGTGGGCCCAAGTGCTGGTGTGTCGCCCTGGGAGCG	252
Db	181	GGACCCGGCGGCTTTCCGGCGGCTTGGTGGGCCCAAGTGCTGGTGTGTCGCCCTGGGAGCG	240
Qy	253	ACGGCGCCCGCCCGCGCCCTCTTCGCCCAAGGTCTCTGCTGAAGAGCTGGTGGC	312
Db	241	ACGGCGCCCGCCCGCGCCCTCTTCGCCCAAGGTCTCTGCTGAAGAGCTGGTGGC	300
Qy	313	CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCAAGACGTGTGTCGCTTCGGCTTCGC	372
Db	301	CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCAAGACGTGTGTCGCTTCGGCTTCGC	360
Qy	373	GCTGCTGGACGGGGCCCCGGGGGCCCCCCCGAGGCCCTTCACCAACACAGCTGGCGACGTA	433
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Qy	673	CTGGAACATAGCTCAGGGAGGCGGGGTCCCCCTGGGCTGCGACCCCGGGTGGGAG	732
Db	661	CTGGAACATAGCTCAGGGAGGCGGGGTCCCCCTGGGCTGCGACCCCGGGTGGGAG	720
Qy	733	GAGCGGGGGGAGTGCCACGCGAAGTGTGCGGTGCCAAGAGGCCCGAGGCGTGGCGC	792
Db	721	GAGCGGGGGGAGTGCCACGCGAAGTGTGCGGTGCCAAGAGGCCCGAGGCGTGGCGC	780
Qy	793	TGCCCTTGACCGAGCGGCGCGTGGCGAGGGGTCTGGGCCACCCGGCGAGGAC	852
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Qy	853	CGGTGACCGAGTGACCGTGGTCTCTGTGTGGTGTACCTGCCACAGCCCGCGAAGAAC	912
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Qy	1033	CCGGGTGTACCGGAGACCAAGCACTTCCTCTACTCTCAAGGACAAAGAGCAGCTGGC	1092
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Db	1081	GCCTCTCTCTACTCAGCTCTCTGAGGGCCCCAGCGTGACTTGGGCTCGGAGGCTCGTGA	1140
Qy	1153	GACATCTTTCTGGGTTCAGGCCCTCGGATGCGAGGGACTCCCGCAGGTTGCCCGGCT	1212
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QY	1213	GCCCCAGCGCTACTGGCAAAATGCGGCCCTTGTTTCTTGAGAGTGCTGGGAACACACGCGCA	1272
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QY	1273	GTGCCCCTACGGGGTGCTCCACAAGACGCACTGCCCGCTGGAGCTGCGGTCAACCCAGC	1332
Db	1261	GTGCCCCTACGGGGTGCTCCACAAGACGCACTGCCCGCTGGAGCTGCGGTCAACCCAGC	1320
QY	1333	AGCCGGTGTCTGTGCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCTTCAGAGCATGTGA	1392
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QY	1393	CACAGACCCCGTCGCCGTGTGTCAGCTGCTCCGCCACACAGCAGCAGCCCCCTGGCAGTGTGA	1452
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Db	1441	CGGCTTCGTGCGGGCTGCCCTGCGCCCGGCTGTGCCCCAGGGCTCTGGGGCTCCAGGCA	1500
QY	1513	CAACGAAGCCGCTTCTCAGGAACACCAAGAAGTTCAATCTCCCTGGGGAAGCATGCGCAA	1572
Db	1501	CAACGAAGCCGCTTCTCAGGAACACCAAGAAGTTCAATCTCCCTGGGGAAGCATGCGCAA	1560
QY	1573	GCTCTCGCTGACGAGCTGACGTGGAAAGATGAGGGTGGGGACTTGCCTTTGGCTGGCGCAG	1632
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QY	1633	GAGCCAGGGTGGCTGTGTTCCGGCCGACAGCACCCGTCTCCGTGAGAGATCCTGGC	1692
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QY	1693	CAAGTTCCTGCACGTGGCTGATGAGTGTGACGTGCTGAGCTGCTCAGGTCTTCTTTTA	1752
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QY	1753	TGTCACGGAGACCAGTTTCAAAAGAACAGGCTCTTTTTTACCGGAAGAGTGTCTGGAG	1812
Db	1741	TGTCACGGAGACCAGTTTCAAAAGAACAGGCTCTTTTTTACCGGAAGAGTGTCTGGAG	1800
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Db	1801	CAAGTTCGAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGTGGGAGCTGTC	1860
QY	1873	GGAACAGAGTCAAGCAGCATCGGGAAGCCAGGCCCGCTGCTGACGTCCAAGATCCG	1932
Db	1861	GGAACAGAGTCAAGCAGCATCGGGAAGCCAGGCCCGCTGCTGACGTCCAAGATCCG	1920
QY	1933	CTTCATCCCAAGCCTGACGGGCTGGCGCGATTGTGAACATGATGATCCTCGTGGAGC	1992
Db	1921	CTTCATCCCAAGCCTGACGGGCTGGCGCGATTGTGAACATGATGATCCTCGTGGAGC	1980
QY	1993	CAGAACGTTCCGCAGAGAAAAGGGCCGAGCGTCTCACTCGAGGGTGAAGGCATGTT	2052
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QY	2053	CAGCGTGTCAACTACAGAGGGGCGCGGCCCTCCTGGCGCCCTCTGTGTGGG	2112
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QY	2173	GCCGCCGTGAGTGTACTTTGTCAAGGTGGATGTGACGGGCGCTAGACACCATCCCCA	2232
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QY	2233	GGACAGGCTACGAGGTCTATCGCCACGATCATCAAAACCCAGAACACGTACTGCGTGG	2292
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; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Apple, Randolph T.
;   REGISTRATION NUMBER: 36,429
;   REFERENCE/DOCKET NUMBER: 015389-0029300S
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 173:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4029 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
;   NAME/KEY:
;   LOCATION: 1..4029
; OTHER INFORMATION: /note= "preliminary sequence for
; OTHER INFORMATION: human TRT cdna insert of
; OTHER INFORMATION: plasmid pGRN121"
; US-08-851-843A-173

Query Match          95.3%; Score 3618.6; DB 3; Length 4029;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 3725; Conservative 0; Mismatches 54; Indels 9; Gaps 8;

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D 61 GCGCGCTCCCGGTGCGGAGCGGTGCGCTCCCTGCTGCGACGCACTACCGGAGTGCT 120
QY 133 GCGCGTGGCGACGTTGCTGCGCGCTGCGGCGCCAGGCTGGCGGCTGGCGCGCG 192
D 121 GCGCGTGGCGACGTTGCTGCGCGCTGCGGCGCCAGGCTGGCGGCTGGCGCGCG 180
QY 193 GGACCGCGCGGCTTTCGCGCGCTGCTGGCGCCAGTGCCTGCTGCTGGCTGGGACGC 252
D 181 GGACCGCGCGGCTTTCGCGCGCTGCTGGCGCCAGTGCCTGCTGCTGGGANGN 240
QY 253 AGCGCGCGCGCGCGCGCGCGCGCTTCCTCGCGCAGGTGCTCGCTGGAAGAGCTGTGCG 312
D 241 ANGGCGCGCGCGCGCGCGCGCGCTTCCTTCGCGCAGGTGCTCGCTGGAANGANC 300
QY 313 CCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGAAGACGTCGTGGCCCTTCGGCTTCGC 372
D 301 CCGAGTGTGTCANANGCTGTGCGANGCGCGCGCGGCGAANACGTCGTGGCCCTTCGGCTTCGC 360
QY 373 GCTGTGGACGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTA 432
D 361 GCTGTGGACGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTA 420
QY 433 CCGTGGCCAAACAGGTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGGCTGCTGCTGG 492
D 421 CCGTGGCCAAACAGGTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGGCTGCTGCTGG 480
QY 493 CCGCGTGGCGACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 552
D 481 CCGCGTGGCGACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 553 GCGTCCAGCTCGGCTACACAGTGTGCGGCGCGCGCGCTGTACACAGCTGGCGCGTCCAC 612
D 541 GNTTCCAGCTCGGCTACACAGTGTGCGGCGCGCGCGCTGTACACAGCTGGCGCGTCCAC 600
QY 613 TCAGGCCGCGCGCGCGCGCGCGCGCTAGTGGACCCCGAAGGCGCTCGGGATGCGAAGCGGC 672
D 601 TCAGGCCGCGCGCGCGCGCGCGCGCTANTGGA-CCCGAANGCGCTCTGGGAT-CCACGGGC 658
QY 673 CTGGAACCATAGCTCAGGAGCGCGGGGTCCCGCTGGCGCTGGCAGCCCGCGGTCGAG 732
D 1734 TATGTCACGAGACACGCTTTTCAAGAAAGACAGGCTCTTTTCTACCGGAAGAGTGCTGG 1793
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Db 659 CTGGAACCATAGCTCAGGAGAGCCGGGGTCCCGCTGG-CTGCCACCCCGGGTGCAG 717
QY 733 GAGCGCGGGGCGAGTGCACAGCCGAAGTCTGCGGTTGCCCAAGAGGCCACAGGCTGGCGC 792
D 718 GAGCGCGGGGCGAGTGCACAGCCGAAGTCTGCGGTTGCCCAAGAGGCCACAGGCTGGCGC 777
QY 793 TGCCCTGTAGCGCGGAGCGGACGCCCTTGGGCGAGGGGTCTTGGGCCACCCCGGCGAGGAC 852
D 778 TGCCCTGTAGCGCGGAGCGGACGCCCTTGGGCGAGGGGTCTTGGGCCACCCCGGCGAGGAC 837
QY 853 GCGTGCACCGAGTGACCGGTGGTTCTGTGTGTGTACCTGCCAGACCCCGGCGAAGC 912
D 838 GCGTGCACCGAGTGACCGGTGGTTCTGTGTGTGTACCTGCCAGACCCCGGCGAAGC 897
QY 913 CACCTCTTTGGAGGTGCGCTCTGTGGCAGCGGCCACTCCACCCATCCGTGGGCGGCCCA 972
D 898 CACCTCTTTGGAGGTGCGCTCTGTGGCAGCGGCCACTCCACCCATCCGTGGGCGGCCCA 957
QY 973 GCACACGCGGGGCCCCCATCCACATCGCGGCCACACGTCCTTGGGACACGCTTTGTTC 1032
D 958 GCACACGCGGGGCCCCCATCCACATCGCGGCCACACGTCCTTGGGACACGCTTTGTTC 1016
QY 1033 CCGCGTGTAGCGCGGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGAGAGCTGG 1092
D 1017 CCGCGTGTAGCGCGGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGNA--CACTGGC 1074
QY 1093 GCGCTCTTCTACTCT-AGCTCTCTGAGCGCCAGCTGCTGCGCTCGGAGGCTCGTGG 1151
D 1075 NCCCTCTTCTACTCAATATATCTGAGGCCACGCTGACTGCGGTTCGGAGGTTCTGGT 1134
QY 1152 AGACCATCTTTCTGGGTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCGCGC 1211
D 1135 GAGACANTCTTCTGTTCCAGGCCCTGGATGCCA-GGATTCCCGCAGGTTGCCCGCGC 1193
QY 1212 TGCCCGCAGGCTACTGGCAATAGCGGCCCTCTTCTGAGCTGCTGGGAAACACGCGC 1271
D 1194 TGCCCGCAGGNTACTGGCAATAGCGGCCCTCTTCTGAGCTGCTGGGAAACACGCGC 1253
QY 1272 AGTGCCCTTACGGGGTCTCTCAAGACGCACTGCGCGCTGCGAGCTGCGGTCAACCCAG 1331
D 1254 AGTGCCCTTACGGGGTCTCTCAAGACGCACTGCGCGCTGCGAGCTGCGGTCAACCCAG 1313
QY 1332 CAGCGGCTGTGTGTCGGGAGAACCCCGAGGGCTCTGTGGCGGCCCGCGAGGAGG 1391
D 1314 CAGCGGCTGTGTGTCGGGAGAACCCCGAGGGCTCTGTGGCGGCCCGCGAGGAGG 1373
QY 1392 -ACACAGACCCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1450
D 1374 AACACAGACCCCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1433
QY 1451 TACGGCTTCTGCGGGCTTGCCTTGCCTGCGCGCTGCTGCGCGCGCTTGGGCTCCAGG 1510
D 1434 TACGGCTTCTGCGGGCTTGCCTTGCCTGCGCGCTGCTGCGCGCGCTTGGGCTCCAGG 1493
QY 1511 CACAAGAACGCGCTTCTCAGGAACACCAAGAGTTTCTCCTTGGGGAAGCATGCC 1570
D 1494 CACAAGAACGCGCTTCTCAGGAACACCAAGAGTTTCTCCTTGGGGAAGCATGCC 1553
QY 1571 AAGCTCTCCTGCGAGAGCTGACGTGGAAAGATGAGCGTGGGAGTGCCTTGGCTGGCG 1630
D 1554 AAGCTCTCCTGCGAGAGCTGACGTGGAAAGATGAGCGTGGGAGTGCCTTGGCTGGCG 1613
QY 1631 AGGAGCCAGGGGTTGGCTGTGTTCCGGCGGAGACACCGCTGCTGAGGAGATCCCTG 1690
D 1614 AGGAGCCAGGGGTTGGCTGTGTTCCGGCGGAGACACCGCTGCTGAGGAGATCCCTG 1673
QY 1691 GCCAAGTTCTCCTGCTGCTGATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1750
D 1674 GCCAAGTTCTCCTGCTGCTGATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1733
QY 1751 TATGTACGAGACACGCTTTTCAAGAAAGACAGGCTCTTTTCTACCGGAAGAGTGTCTG 1810
D 1734 TATGTACGAGACACGCTTTTCAAGAAAGACAGGCTCTTTTCTACCGGAAGAGTGTCTG 1793
```

QY	1811	ACCAAGTTCGAAGCAATGGAAATCAGACAGCACTTGAAGAGGCTCAGCTCGGAGCTG	1870
DB	1794	ACCAAGTTCGAAGCAATGGAAATCAGACAGCACTTGAAGAGGCTCAGCTCGGAGCTG	1853
QY	1871	TCGGAAGCAGAGGTCAGGCAGCATCGGAAGCAGCCCGCCCTGCTGACGTCCAGACTC	1930
DB	1854	TCGGAAGCAGAGGTCAGGCAGCATCGGAAGCAGCCCGCCCTGCTGACGTCCAGACTC	1913
QY	1931	CGCTTCATCCCAAGCTGACGGGCTGCGGCCGATGTGAACATGACTACGTCTGGGA	1990
DB	1914	CGCTTCATCCCAAGCTGACGGGCTGCGGCCGATGTGAACATGACTACGTCTGGGA	1973
QY	1991	GCAGAACTTCGCGAGAGAAAGAGGCGGAGCGCTCACCCTCAGGCTGAAGCACTG	2050
DB	1974	GCAGAACTTCGCGAGAGAAAGAGGCGGAGCGCTCACCCTCAGGCTGAAGCACTG	2033
QY	2051	TTACAGCGTCTCAACTACGAGCGGCGGCGGCCCTCCTGGGGCCCTCTGTGTG	2110
DB	2034	TTACAGCGTCTCAACTACGAGCGGCGGCGGCCCTCCTGGGGCCCTCTGTGTG	2093
QY	2111	GGCTTGAGGATATCCAGAGGCTTGCGGCACCTTCGTGCTGCGTGGGGCCAGGAC	2170
DB	2094	GGCTTGAGGATATCCAGAGGCTTGCGGCACCTTCGTGCTGCGTGGGGCCAGGAC	2153
QY	2171	CGCGCGCTGAGCTGTACTTCTCAAGGTGGATGTGACGGGCGGTACGACACCATCC	2230
DB	2154	CGCGCGCTGAGCTGTACTTCTCAAGGTGGATGTGACGGGCGGTACGACACCATCC	2213
QY	2231	CAGGACGCTCAGGAGGTCTATCGCCAGCATCATCAACCCAGAACACGTACTGCGTG	2290
DB	2214	CAGGACGCTCAGGAGGTCTATCGCCAGCATCATCAACCCAGAACACGTACTGCGTG	2273
QY	2291	CGTCGGTATGCGGTGTCAGAAAGCGCGCCATGAGGACGTCCGGAAGGCTTCAAGAGC	2350
DB	2274	CGTCGGTATGCGGTGTCAGAAAGCGCGCCATGAGGACGTCCGGAAGGCTTCAAGAGC	2333
QY	2351	CACGTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGCTCAGCTGCAG	2410
DB	2334	CACGTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGCTCAGCTGCAG	2393
QY	2411	GAGACAGCGCTCAGGAGTCCGCTGCTATCGAGCAGAGCTCCTCCTGATGAGGCC	2470
DB	2394	GANAACAGCCGCTCAGGAGTCCGCTGCTATCGAGCAGAGCTCCTCCTGATGAGGCC	2453
QY	2471	AGCAGTGGCTCTTCGAGCTCTTCCTACGTTTATGTCGACACCGCGCTGCGCATCAGG	2530
DB	2454	AGCAGTGGCTCTTCGAGCTCTTCCTACGTTTATGTCGACACCGCGCTGCGCATCAGG	2513
QY	2531	GGCAAGTCTACGTCCAGTCCAGGGATCCCGAGGCTCCATCTCTCCAGCTGCTC	2590
DB	2514	GGCAAGTCTACGTCCAGTCCAGGGATCCCGAGGCTCCATCTCTCCAGCTGCTC	2573
QY	2591	TGCAGCCTGTGTACGGGACATGGAGAACAGCTGTTTTCGGGGATTCGGCGGACGGG	2650
DB	2574	TGCAGCCTGTGTACGGGACATGGAGAACAGCTGTTTTCGGGGATTCGGCGGACGGG	2633
QY	2651	CTGCTCTGCGTTTGGTGATGATTTCTTGTGTTGACACCTCACTCACCCACGCGAAA	2710
DB	2634	CTGCTCTGCGTTTGGTGATGATTTCTTGTGTTGACACCTCACTCACCCACGCGAAA	2693
QY	2711	ACCTTCTCAGACCTTGTTCGAGGTCTCCCTGAGTATGGCTGGGTGAATTTGGG	2770
DB	2694	ACCTTCTCAGACCTTGTTCGAGGTCTCCCTGAGTATGGCTGGGTGAATTTGGG	2753
QY	2771	AAGACAGTGGTGAATCTCCTCTAGAAGCAGGCGCTGGGTGGACGGCTTTTGTTCAG	2830
DB	2754	AAGACAGTGGTGAATCTCCTCTAGAAGCAGGCGCTGGGTGGACGGCTTTTGTTCAG	2813
QY	2831	ATGCGCGCCACGGCTATTCCTGCTGGTGGCGCTGCTGCTGATACCGGACCTGGAG	2890
DB	2814	ATGCGCGCCACGGCTATTCCTGCTGGTGGCGCTGCTGCTGATACCGGACCTGGAG	2873

QY	2891	GTGAGAGCGACTACTCTCAGCTATGCCGAGCTTCCATCAGAGCCAGTCTCAGCTTCAAC	2950
DB	2874	GTGAGAGCGACTACTCTCAGCTATGCCGAGCTTCCATCAGAGCCAGTCTCAGCTTCAAC	2933
QY	2951	CGCGGCTTCAAGGCTGGGAGAACATGCTGCAAACTCTTTGGGCTTTGGGCTGAAG	3010
DB	2934	CGCGGCTTCAAGGCTGGGAGAACATGCTGCAAACTCTTTGGGCTTTGGGCTGAAG	2993
QY	3011	TGTCACAGCCTGTTCTTGATTTGAGGTGAACAGCCTCAGACGGTGTGACCAACATC	3070
DB	2994	TGTCACAGCCTGTTCTTGATTTGAGGTGAACAGCCTCAGACGGTGTGACCAACATC	3053
QY	3071	TACAAGATCCTCTGCTGAGGCTTACAGGTTTCAAGCATGCTGCTGAGCTTCCATTT	3130
DB	3054	TACAAGATCCTCTGCTGAGGCTTACAGGTTTCAAGCATGCTGCTGAGCTTCCATTT	3113
QY	3131	CATCAGCAAGTTTGAAGAACCCCATTTTCTCGCGCTCATCTCTGACACGGCTCC	3190
DB	3114	CATCAGCAAGTTTGAAGAACCCCATTTTCTCGCGCTCATCTCTGACACGGCTCC	3173
QY	3191	CTCTGCTACTCTTCTGAAAGCAAGAACGAGGATGTGCTGGGGCCCAAGGGCGCC	3250
DB	3174	CTCTGCTACTCTTCTGAAAGCAAGAACGAGGATGTGCTGGGGCCCAAGGGCGCC	3233
QY	3251	GGCGGCTCTGCTCTCCGAGCGGTGCTGCTGCAACCAAGCATTTCTGCTCAAG	3310
DB	3234	GGCGGCTCTGCTCTCCGAGCGGTGCTGCTGCAACCAAGCATTTCTGCTCAAG	3293
QY	3311	CTGACTCGACACCGTGTACCTACGTGCGACCTCTGCGGCTCATCTCAGGACAGCCAGG	3370
DB	3294	CTGACTCGACACCGTGTACCTACGTGCGACCTCTGCGGCTCATCTCAGGACAGCCAGG	3353
QY	3371	CAGCTGAGTTCGAAAGTCCCGGGAGCGCTGCTGCTGAGGCGCGAGCCGAACCCG	3430
DB	3354	CAGCTGAGTTCGAAAGTCCCGGGAGCGCTGCTGCTGAGGCGCGAGCCGAACCCG	3413
QY	3431	GCAGTGCCTCTCAGACTTCAAGACCATTCCTGAGTGTGATGCGCCACCCACAGCCAGG	3490
DB	3414	GCAGTGCCTCTCAGACTTCAAGACCATTCCTGAGTGTGATGCGCCACCCACAGCCAGG	3473
QY	3491	GAGACAGACACAGCAGCCCTGTACGCGCGGCTCTAGCTCCAGGGAGGAGGGCGG	3550
DB	3474	GAGACAGACACAGCAGCCCTGTACGCGCGGCTCTAGCTCCAGGGAGGAGGGCGG	3533
QY	3551	CCACACCCAGCGCGCAGCCTGAGGTCTGAGGCTTGAAGTGTGCTGAGGCTTGAAGTGTG	3610
DB	3534	CCACACCCAGCGCGCAGCCTGAGGTCTGAGGCTTGAAGTGTGCTGAGGCTTGAAGTGTG	3593
QY	3611	TGCATGTCGCGCTGAGGCTGAGTTCGCGCTGAGGCTTGAAGTGTGCTGAGGCTTGAAGTGTG	3670
DB	3594	TGCATGTCGCGCTGAGGCTGAGTTCGCGCTGAGGCTTGAAGTGTGCTGAGGCTTGAAGTGTG	3653
QY	3671	CTGAGTGTCCAGCACACCTTGCCTTCTACTTCCACACAGGCTGCGGCTCCAGCC	3730
DB	3654	CTGAGTGTCCAGCACACCTTGCCTTCTACTTCCACACAGGCTGCGGCTCCAGCC	3713
QY	3731	CAGGGCAGCTTTTCTTCCACAGGCGCGGCTTCCACTCCCCACATAGGAATAGTCCAT	3790
DB	3714	CAGGGCAGCTTTTCTTCCACAGGCGCGGCTTCCACTCCCCACATAGGAATAGTCCAT	3773
QY	3791	CCCCGAT 3798	
DB	3774	CCCCGAT 3781	

## RESULT 13

US-08-974-549A-292  
; Sequence 292, Application US/08974549A  
; Patent No. 6166178  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru



Qy	1033	CCCCGTGTACGCCGAGACCAAGCACTTCTCTACTCTCTCAGGGGACAAAGAGCAGCTGCG	1099
Db	1017	CCCCGTGTACGCCGAGACCAAGCACTTCTCTACTCTCTCAGGGGACCAAGNA--CACTGCG	1074
Qy	1093	GCCCTCCTTCTACTC-AGTCTCTGAGGCCAGCCTGACTGGCGCTCGAGGCTCGTGG	1151
Db	1075	NCCCTCTTCTACTCAATATATCTGAGGCCAGCCTGACTGGCGTTCTGGAGGTTGCGT	1134
Qy	1152	AGACCATTTTCTTGGGTTCAGGCCCTTGGATGCCAGGACTTCCCCGAGGTTGCCCGGCC	1211
Db	1135	GAGACANTCTTTCTTGGTTCCAGGCCTTGGATGCCA-GGATTCCCGCGAGTTGCCCGGCC	1193
Qy	1212	TGCCCCAGCGCTACTTGCAGAAATGGGGCCCTGTTFCTGGAGCTGTCTTGGGAAACACGCGC	1271
Db	1194	TGCCCCAGCGNTACTTGCAGAAATGGGGCCCTGTTFCTTCTGGAGCTGTCTTGGGAAACACGCGC	1253
Qy	1272	AGTCCCTTACGGGGTCTCTCTCAAGACGACATGCCCGCTGCCAGCTGCCGCTCACCCAG	1331
Db	1254	AGTGCCCTTACGGGGTGTTCCTCAAGACGACATGCCCGCTTGGAGCTTCCGGTCAACCCAG	1313
Qy	1332	CAGCGGTGTCTGTGCCGGGAGAACCCAGAGGCTCTGTGGGGCCCCCGAGGAGGAGG	1391
Db	1314	CAGCGGTGTCTGTGCCGGGAGAACCCAGAGGCTCTGTGGGGCCCCCGAGGAGGAGG	1373
Qy	1392	-ACACAGACCCCGTCCGCTGTGTGCTGCTCGCCAGCACAGCAGCAGCCCTGGCAGGTG	1450
Db	1374	AACACAGACCCCGTCCGCTGTGTGCTGCTCGCCAGCACAGCAGCAGCCCTGGCAGGTG	1433
Qy	1451	TAGGGCTTCTGGGGCTCGCTCGCGCGGCTGTGTGCCCGCCAGGCTCTTGGGCTCCAGG	1510
Db	1434	TAGGGCTTCTGGGGCTCGCTGTGTGCCCGGCTGTGTGCCCGCCAGGCTCTTGGGCTCCAGG	1493
Qy	1511	CACAACGAAGCGCGCTTCTCTCAGGAACACCAAGAGTTCTATCTCCCTGGGGAAAGCATGCC	1570
Db	1494	CACAACGAAGCGCGCTTCTCTCAGGAACACCAAGAGTTCTATCTCCCTGGGGAAAGCATGCC	1553
Qy	1571	AAGCTCTCGTGCAGGAGCTGACGTGGAAGATGAGCGTGGGAGCTGCCTTGGCTGCGC	1630
Db	1554	AAGCTCTCGTGCAGGAGCTGACGTGGAAGATGAGCGTGGGAGCTGCCTTGGCTGCGC	1613
Qy	1631	AGGAGCCACGGGTGTGGCTGTGTTCGGGCGCAGACACCGTCTGGGTGAGGAGATCCTG	1690
Db	1614	AGGAGCCACGGGTGTGGCTGTGTTCGGGCGCAGACACCGTCTGGGTGAGGAGATCCTG	1673
Qy	1691	GCCAAAGTCTGCAGCTGGCTGATGAGTGTGTACGTGCTCGAGCTGTCTCAGGCTCTTCTTT	1750
Db	1674	GCCAAAGTCTGCAGCTGGCTGATGAGTGTGTACGTGCTCGAGCTGTCTCAGGCTCTTCTTT	1733
Qy	1751	TATGTACGAGAGACCGTTTCAAAGAACAGAGCTCTTTTTCTACCGGAAGATGTCTGG	1810
Db	1734	TATGTACGAGAGACCGTTTCAAAGAACAGAGCTCTTTTTCTACCGGAAGATGTCTGG	1793
Qy	1811	AGCAAGTTGCAAGCATTGAATCAGACACACTTGAAGAGGTGTCAGCTGCCGGAGCTG	1870
Db	1794	AGCAAGTTGCAAGCATTGAATCAGACACACTTGAAGAGGTGTCAGCTGCCGGAGCTG	1853
Qy	1871	TCGGAAGCAGAGTTCAGGCAGCATTCGGGAAGCAGGCCCGCTGTGTAGCTCCAGACTC	1930
Db	1854	TCGGAAGCAGAGTTCAGGCAGCATTCGGGAAGCAGGCCCGCTGTGTAGCTCCAGACTC	1913
Qy	1931	CGCTTCATCCCAAGCCTGTACAGCGGCTGCGGCCGATGTGAACTAGGACTACGTCTGGGA	1990
Db	1914	CGCTTCATCCCAAGCCTGTACAGCGGCTGCGGCCGATGTGAACTAGGACTACGTCTGGGA	1973
Qy	1991	GCCAGACGTTCCGAGAGAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACCTG	2050
Db	1974	GCCAGACGTTCCGAGAGAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACCTG	2033
Qy	2051	TTCAGCGTGTCAACTACGAGCGGGCGCGGCCCGGCTCTCTTGGGCGCTCTGTGCTG	2110
Db	2034	TTTACGCGTGTCAACTACGAGCGGGCGCGGCCCGGCTCTCTTGGGCGCTCTGTGCTG	2093
Qy	2111	GGCCTGGACGATATCCACAGGGGCTTGGCGCACCTTGTGTGCTGCTGTGGGGCCCCAGGAC	2170

Db	2094	 GGCCTGGACGATATCCACAGGGCGTGGCGCACCTTCTGTGCTGTGTGGGGGCCAGGAC	2153
QY	2171	CCGCGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGGTACGACACCATCCCC	2230
Db	2154	CCGCGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGGTACGACACCATCCCC	2213
QY	2231	CAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGTG	2290
Db	2214	CAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGTG	2273
QY	2291	CGTCGGTATGCGGTGTCCAGAAGCGCGCCCATGGGCACGTCCGCAAGCGCTTCAAGAGC	2350
Db	2274	CGTCGGTATGCGGTGTCCAGAAGCGCGCCCATGGGCACGTCCGCAAGCGCTTCAAGAGC	2333
QY	2351	CACGTCCTACCTTGTACAGACCTCCAGCGCTACATGGGACAGTTCGTGGCTACCTGCAG	2410
Db	2334	CACGTCCTACCTTGTACAGACCTCCAGCGCTACATGGGACAGTTCGTGGCTACCTGCAG	2393
QY	2411	GAGACAGCGCGTGTAGGGATGCGCTCGTCATCGAGCAGAGCTCTCCCTGAATGAGGCC	2470
Db	2394	GANAACAGCGCGTGTAGGGATGCGCTCGTCATCGAGCAGAGCTCTCCCTGAATGAGGCC	2453
QY	2471	AGCAGTGGCGCTTTCGACAGCTTTCCTTACGCTTATGTGCCACACCGCTGCGCATCAGG	2530
Db	2454	AGCAGTGGCGCTTTCGACAGCTTTCCTTACGCTTATGTGCCACACCGCTGCGCATCAGG	2513
QY	2531	GGCAAGTCCCTACGTCFACGCGGACATGGAGAACAAAGCTGTTGCGGGGATTGCGGGGACGGG	2590
Db	2514	GGCAAGTCCCTACGTCFACGCGGACATGGAGAACAAAGCTGTTGCGGGGATTGCGGGGACGGG	2573
QY	2591	TGCAGCCTGTGCTACGCGCGACATGGAGAACAAAGCTGTTGCGGGGATTGCGGGGACGGG	2650
Db	2574	TGCAGCCTGTGCTACGCGCGACATGGAGAACAAAGCTGTTGCGGGGATTGCGGGGACGGG	2633
QY	2651	CTGCTCTCGGTTTGTGGATGATTTCTTGTGGTACACCTCACCTCACCCACCGGAAA	2710
Db	2634	CTGCTCTCGGTTTGTGGATGATTTCTTGTGGTACACCTCACCTCACCCACCGGAAA	2693
QY	2711	ACCTTCCTCAGGACCCGTGGTCCGAGGTGTCCTCTGAGTATGGCTGCGTGTGTAACCTTGGG	2770
Db	2694	ACCTTCCTCAGGACCCGTGGTCCGAGGTGTCCTCTGAGTATGGCTGCGTGTGTAACCTTGGG	2753
QY	2771	AAGACAGTGTGTAACCTTCCCTGTAGAAGACGAGCGCCTGGGTGGCAGCGCTTTGTTCAG	2830
Db	2754	AAGACAGTGTGTAACCTTCCCTGTAGAAGACGAGCGCCTGGGTGGCAGCGCTTTGTTCAG	2813
QY	2831	ATGCCGGCCACAGGCCATTTCCCTGTGTGCGGCTGCTGCTGGATACCCGGACCCCTGGAG	2890
Db	2814	ATGCCGGCCACAGGCCATTTCCCTGTGTGCGGCTGCTGCTGGATACCCGGACCCCTGGAG	2873
QY	2891	GTGCAGAGGACACTACCGCATATGCCCGACCTCCATCAGAGCCAGTCTCACCTTCAAC	2950
Db	2874	GTGCAGAGGACACTACCGCATATGCCCGACCTCCATCAGAGCCAGTCTCACCTTCAAC	2933
QY	2951	CGCGGCTTCAAGGCTGGGAGGAACATCGCTGCGAAACTCTTTGGGCTCTTTGGCGCTGAAG	3010
Db	2934	CGCGGCTTCAAGGCTGGGAGGAACATCGCTGCGAAACTCTTTGGGCTCTTTGGCGCTGAAG	2993
QY	3011	TGTGCACAGCCTGTTTCGGATTTGCAGGTGAACAGCCTCCAGACGCTGTGCACCAACATC	3070
Db	2994	TGTGCACAGCCTGTTTCGGATTTGCAGGTGAACAGCCTCCAGACGCTGTGCACCAACATC	3053
QY	3071	TACAAGATCCTCTGCTGCAGGGGTACAGGTTTTCACGCATGTGCTGCAGCTCCCATTT	3130
Db	3054	TACAAGATCCTCTGCTGCAGGGGTACAGGTTTTCACGCATGTGCTGCAGCTCCCATTT	3113
QY	3131	CATCAGCAAGTTTGGAGAACCCACATTTTTCTCGGGTCTATCTGCACAGGCGCTCC	3190
Db	3114	CATCAGCAAGTTTGGAGAACCCACATTTTTCTCGGGTCTATCTGCACAGGCGCTCC	3173
QY	3191	CTCTGCTACTCCATCTCTGAAAGCCAAAGACGCAAGGATGTGCTGGGGGCCAAGGCGCC	3250

Db	3174	CTCTGTACTTCCATCTCTGAAAGCCAGACGCGAGGGATGTCTGTGGGGGCCAAGGGCGCC	3333
Qy	3251	GCGGGGCCTCTGGCCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCATTTCTTCTCTCAAG	3310
Db	3234	GCGGGGCCTCTGGCCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCATTTCTTCTCTCAAG	3293
Qy	3311	CTGACTGACACCGTGTACCTTACGTGGCCACTCTCTGGGGTCTCTCAGGACAGCCCAAGCG	3370
Db	3294	CTGACTCGACACCGTGTACCTTACGTGGCCACTCTCTGGGGTCTCTCAGGACAGCCCAAGCG	3353
Qy	3371	CAGCTGAGTCGGAAAGCTCCCGGGGACGACTGACCTGCCTTGAGGCGCCGAGCCCAACCCG	3430
Db	3354	CAGCTGAGTCGGAAAGCTCCCGGGGACGACTGACCTGCCTTGAGGCGCCGAGCCCAACCCG	3413
Qy	3431	GCACTGCCCTCAGACTTCAAGACCATCTCTGGACTGATGGCCACCGCCACAGCCCAAGGCC	3490
Db	3414	GCACTGCCCTCAGACTTCAAGACCATCTCTGGACTGATGGCCACCGCCACAGCCCAAGGCC	3473
Qy	3491	GAGAGCAGACACAGCAGCCCTCTCAGCGCGGGCTCTACCTCCAGGGAGGGAGGGCGG	3550
Db	3474	GAGAGCAGACACAGCAGCCCTCTCAGCGCGGGCTCTACCTCCAGGGAGGGAGGGCGG	3533
Qy	3551	CCACACCCAGGCGCCGACCGCTGGAGTCTGAGGGCTGAGTCAGTCTTTGGCCGAGGCC	3610
Db	3534	CCACACCCAGGCGCCGACCGCTGGAGTCTGAGGGCTGAGTCAGTCTTTGGCCGAGGCC	3593
Qy	3611	TGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGGCTGAGCGCCCAAGGG	3670
Db	3594	TGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGGGCTGAGCGCCCAAGGG	3653
Qy	3671	CTGAGTGTCCAGACACACTTCGGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCC	3730
Db	3654	CTGAGTGTCCAGACACACTTCGGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCC	3713
Qy	3731	CAGGGCCAGTCTTTCTCCACAGGAGCCCGCTTCCACTCCCCACATAGGAATAGTCCAT	3790
Db	3714	CAGGGCCAGTCTTTCTCCACAGGAGCCCGCTTCCACTCCCCACATAGGAATAGTCCAT	3773
Qy	3791	CCOCTGAT	3798
Db	3774	CCCCAGAT	3781

RESULT 14  
US-08-854-050-173  
; Sequence 173, Application US/08854050  
; Patent No. 6261836  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: No. 6261836el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/854,050  
; FILING DATE: 09-MAY-1997  
; CLASSIFICATION: 536







**Matches 3725; Conservative 0; Mismatches 54; Indels 9; Gaps 8;**

QY	13	GCAGCGTGGGTCTCTGCTGCGACAGTGGGAAGCCCTGGCCCGCGCCACACCCCGCGATGCC	72
DB	1	GCAGCGTGGGTCTCTGCTGCGACAGTGGGAAGCCCTGGCCCGCGCCACACCCCGCGATGCC	60
QY	73	GGGGCTCCCGCTGCGGAGCGGTGCGCTCCCTGCTGCGGACGACACTACCGCGAGGTGCT	132
DB	61	GGCGGTCCCGCTGCGGAGCGGTGCGCTCCCTGCTGCGGACGACACTACCGCGAGGTGCT	120
QY	133	GGCGTGGCCACGTTCTGTGGCGGCCCTGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG	192
DB	121	GGCGTGGCCACGTTCTGTGGCGGCCCTGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG	180
QY	193	GGACCCGGCGCTTTCCGCGCGCTGGTGGCCAGTGCCTGGTGTGCTGGCCCTGGGAGCG	252
DB	181	GGACCCGGCGCTTTTCGCGCGNTGGTGGCCANTGNTGGTGTGCTGGCCCTGGGANGN	240
QY	253	ACGGCGCCCGCCCGCCCTCTCTTCGCGCAGGTGTCTGCTGAAGAGCTGTGTGGC	312
DB	241	ANGGNGCCCGCCCGCCCTCTTTCGCGCAGGTGTCTGCTGAAGANGCTGTGTGGC	300
QY	313	CCGAGTCTGCAGAGGCTGTGCGAGCGGCGGCGAAGACGTGCTGGCTTCGGCTTCGC	372
DB	301	CCGAGTCTGCANANGCTGTGCGANCGGCGCGAANACGTGTGGCTTCGGCTTCGC	360
QY	373	GCTGCTGGAGCGGGCCCGCGGGGCCCTTCACGAGGCTTCACCAACAGCGTGGCAGCTA	432
DB	361	GCTGCTGGAGCGGGCCCGCGGGGCCCTTCACGAGGCTTCACCAACAGCGTGGCAGCTA	420
QY	433	CTGTGCCCAACACGGTGAACGACGACATGCGGGGGAGCGGGCGTGTGCTGCTGCG	492
DB	421	CCTGCCCAACACGCTGACCGACGACATGCGGGGGAGCGGGCGTGTGCTGCTGCG	480
QY	493	CCGCTGGCGGACGACGTGTGTTACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGT	552
DB	481	CCGCTGGCGGACGACGTGTGTTACCTGCTGGCACGCTGCGCGCTTTTGTGCTGGT	540
QY	553	GGTCTCCAGCTTGCGCTTACCAGTGTGCGGGCGCGCTGTACCAGCTCGGCGCTGCCAC	612
DB	541	GGNTCCAGCTTGCGCTTACCANGTGTGCGGGCGCGCTGTACCAGCTCGGCGCTGCNAC	600
QY	613	TCAGGCCGGCGCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAAGCGG	672
DB	601	TCAGGCCGGCGCCCGCCACACGCTANTGGA-CCCGAANGCGTCTGGAT-CCAAACGGC	658
QY	673	CTGGAACCATAGCGTCAAGGAGCGGGGTCCCGCTGGCGCTGCCAGCCCGGGTGGAG	732
DB	659	CTGGAACCATAGCGTCAAGGAGCGGGGTCCCGCTGGG-CTGGACCCCGGGTGGAG	717
QY	733	GAGCGCGGGGGAGTGCCACGCGAAGTCTGCGCTTGCCCAAGAGGCCAGCGCTGGCG	792
DB	718	GAGCGCGGGGAGTCCAGCCAACTCTGCGTTCGCCAAGAGGCCAGCGTGGCG	777
QY	793	TGCCCTGAGCCGGAGCGGACGCCGTGTGGCAGGGTCTGTGGGCCACCCGGGACGAC	852
DB	778	TGCCCTTGAGCCGGAGCGGACGCCGTGTGGCAGGGTCTGTGGGCCACCCGGGACGAC	837
QY	853	CGCTGGACCGAGTACCGTGGTCTGTGTGCTGCTACCTGCCAGACCCGCCGAAGAC	912
DB	838	GCCTGGACCGAGTACCGTGGTCTGTGTGCTGCTACCTGCCAGACCCGCCGAAGAC	897
QY	913	CACCTCTTTGGAGGGTGGCTCTGTGGACCGCGCACTGCCACCCATCCGTGGGCGCGCA	972
DB	898	CACCTCTTTGGAGGGTGGCTCTGTGGACCGCGCACTGCCACCCATCCGTGGGCGCGCA	957
QY	973	GCACCGCGGGCCCCCATCCACATCGCGGCCACACGTCCTTGGGACGACGCTTGTC	1032
DB	958	GCACCGCGGGCCCCCATCCACATCGCGGCCACACGTCCTTGGGACGACGCTTGTC	1016
QY	1033	CCGGGTGACCGGAGACCAAGCACTTCTCTACTCTCAGGCGACAAAGGACGACTGCG	1092
DB	1017	CCGGGTGACCGGAGACCAAGCACTTCTCTACTCTCAGGCGACCAAGNA-CACTGCG	1074

QY	1093	GCCCTCTCTCTACTC-AGCTCTCTGAGGCCAGCCTGACTGCGCTCGAGGCTCTGTGG	1155
Db	1075		1134
QY	1152	AGACCACTTTCTGSGTTCCAGGCGCTTGAGTCCAGGAGCTCCCGCAGGTTCGCCCGC	1211
Db	1135		1193
QY	1212	TGCCCCAGCGCTACTTGGCAAAATGGGCCCTCTTTCTTGAGCTGCTTTGGAAACACAGCGC	1271
Db	1194	TGCCCCAGCGNACTTGGCAAAATGGGCCCTCTTTCTTGAGCTGCTTTGGAAACACAGCGC	1253
QY	1272	AGTGGCCCTAGGGGTGCTCCTCAAGACGACACTGCCGCTGCGAGCTGCGGTCACCCCAG	1331
Db	1254	AGTGGCCCTAGGGGTGCTCCTCAAGACGACACTGCCGCTGCGAGCTGCGGTCACCCCAG	1313
QY	1332	CAGCGGTGTCTGTGCCGGGAGAACCCAGAGGCTCTGTGGGGCCCCCGAGGAGGAGG	1391
Db	1314	CAGCGGTGTCTGTGCCGGGAGAACCCAGAGGCTCTGTGGGGCCCCCGAGGAGGAGG	1373
QY	1392	-ACACAGACCCCTCGCTGTGTGTGCTGCTCGCCAGCACAGACAGACGCCCTTGGCAGGTG	1450
Db	1374	AACACAGACCCCTCGCTGTGTGTGCTGCTCGCCAGCACAGACAGACGCCCTTGGCAGGTG	1433
QY	1451	TACGGCTTGTGTGGGGCTGCTCGCGCGGCTGTGTGCCCGCCCCAGGCTCTGGGCTCCAGG	1510
Db	1434	TACGGCTTGTGTGGGGCTGCTCGCGCGGCTGTGTGCCCGCCCCAGGCTCTGGGCTCCAGG	1493
QY	1511	CACAACGACGCCCTTCTCTCAGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCC	1570
Db	1494	CACAACGACGCCCTTCTCTCAGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCC	1553
QY	1571	AAGCTCTCGTGCAGGAGCTGAGTGAAGATGAGCGTGGGACATGCGCTTGGCTGCGC	1630
Db	1554	AAGCTCTCGTGCAGGAGCTGAGTGAAGATGAGCGTGGGACATGCGCTTGGCTGCGC	1613
QY	1631	AGGAGCCACAGGGTTGCTGTGTTCGGCGCGCAGACAGCAGCTGCTGCTGAGGAGATCCTG	1690
Db	1614	AGGAGCCACAGGGTTGCTGTGTTCGGCGCGCAGACAGCAGCTGCTGCTGAGGAGATCCTG	1673
QY	1691	GCCAAGTTCCTGCACTGGCTGATGAGTGTAGTCTGTCAGCTGCTCAGGTCTTCTTTT	1750
Db	1674	GCCAAGTTCCTGCACTGGCTGATGAGTGTAGTCTGTCAGCTGCTCAGGTCTTCTTTT	1733
QY	1751	TATGTACGGAGACACAGCTTTCAAAAGAACAGGCTTTTTCACCGGAAGAGTGTCTGG	1810
Db	1734	TATGTACGGAGACACAGCTTTCAAAAGAACAGGCTTTTTCACCGGAAGAGTGTCTGG	1793
QY	1811	AGCAAGTTGCMAAGCATTGGNATCAGACAGCACTTGAAGAGGTGTCAGCTGCGGAGCTG	1870
Db	1794	AGCAAGTTGCMAAGCATTGGNATCAGACAGCACTTGAAGAGGTGTCAGCTGCGGAGCTG	1853
QY	1871	TCGGAAGCAGAGGTCAGGACATCTGGGAAGACAGGCCCGCTGCTGCTGAGCTCCAGACTC	1930
Db	1854	TCGGAAGCAGAGGTCAGGACATCTGGGAAGACAGGCCCGCTGCTGCTGAGCTCCAGACTC	1913
QY	1931	CGCTTCATCCCCAAGCTGACGGGCTCGGCCGATGTGTAACATGGACTACGTCTGTGGGA	1990
Db	1914	CGCTTCATCCCCAAGCTGACGGGCTCGGCCGATGTGTAACATGGACTACGTCTGTGGGA	1973
QY	1991	GCCAGAACGTTCCGACAGAAAGAGGGCGAGGCTCTCACCCTGAGGGTGAAGGCACCTG	2050
Db	1974	GCCAGAACGTTCCGACAGAAAGAGGGCGAGGCTCTCACCCTGAGGGTGAAGGCACCTG	2033
QY	2051	TTACGCGTGTCAACTACGACGGGCGGGCGGCCGCTCTCTGGGCGCTCTGTGCTG	2110
Db	2034	TTACGCGTGTCAACTACGACGGGCGGGCGGCCGCTCTCTGGGCGCTCTGTGCTG	2093
QY	2111	GGCCTGACGAGATTCACACAGGCTCGGCGACCTTCTGTGCTGTGCTGTGCGGGCCAGGAC	2170
Db	2094	GGCCTGACGAGATTCACACAGGCTCGGCGACCTTCTGTGCTGTGCTGTGCGGGCCAGGAC	2153



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OM nucleic - nucleic search, using sw model

Run on: October 7, 2003, 08:32:46 ; Search time 214.058 Seconds  
(without alignments)  
10736.958 Million cell updates/sec

Title: US-08-951-733-13\_COPY\_1920\_2820

Perfect score: 901  
Sequence: 1 GTCCAGACTCCGCTTCATCC.....AGGCCCTGGTGGCAGCGCT 901

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1708419 seqs, 1275431651 residues

Total number of hits satisfying chosen parameters: 3416838

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications, NA:\*
- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
  - 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
  - 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
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  - 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
  - 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
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  - 16: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
  - 17: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	901	100.0	1314	14	US-10-294-778-9		Sequence 9, Appli
2	901	100.0	1866	14	US-10-294-778-11		Sequence 11, Appl
3	901	100.0	3396	10	US-09-749-728B-32		Sequence 32, Appl
4	901	100.0	3453	14	US-10-205-629-1		Sequence 1, Appli
5	901	100.0	4015	9	US-09-733-294A-3		Sequence 3, Appli
6	901	100.0	4015	10	US-09-990-080-1		Sequence 1, Appli
7	901	100.0	4015	10	US-09-843-676-224		Sequence 224, App
8	901	100.0	4015	10	US-09-953-052-1		Sequence 1, Appli
9	901	100.0	4015	14	US-10-053-758-224		Sequence 224, App
10	901	100.0	4015	14	US-10-208-243-1		Sequence 1, Appli
11	901	100.0	4015	14	US-10-054-295-224		Sequence 224, App
12	901	100.0	4015	14	US-10-054-611-224		Sequence 224, App
13	901	100.0	4015	14	US-10-105-963-1		Sequence 1, Appli
14	901	100.0	4015	14	US-10-044-692-1		Sequence 1, Appli
15	901	100.0	4015	14	US-10-044-539-1		Sequence 1, Appli
16	901	100.0	8742	12	US-10-105-616-6		Sequence 6, Appli

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ALIGNMENTS

RESULT 1

US-10-294-778-9  
; Sequence 9, Application US/10294778  
; Publication No. US20030060417A1  
; GENERAL INFORMATION:  
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA  
; TITLE OF INVENTION: No. US20030060417A1e1 Gene Having Reverse Transcriptase Motif  
; FILE REFERENCE: 46124-5034-US  
; CURRENT APPLICATION NUMBER: US/10/294,778  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US/09/582,924  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: JP 10/13232  
; PRIOR FILING DATE: 1998-01-08  
; PRIOR APPLICATION NUMBER: JP 10/33584  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: JP 10/139177  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: PCT/JP99/00039  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 13  
; SEQ ID NO 9  
; LENGTH: 1314  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION:  
US-10-294-778-9

Query Match 100.0%; Score 901; DB 14; Length 1314;  
Best Local Similarity 100.0%; Pred. No. 5.7e-242;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGGCTCGCGCGGATTTGTGAACATGGACTA 60  
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Db 324 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGGCTCGCGCGGATTTGTGAACATGGACTA 383  
QY 61 CGTCGTGGAGGCCAGAACGCTTCGGCAGAAAAGAGGCCGCCGCTCCTCAGGCT 120  
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Db 384 CGTCTGGGAGCCAGAACGTTCCGACAGAAAAAGAGGGCCGAGCGTCTACCTCGAGGGT 443  
Qy 121 GAAGGCACTGTTCAGCGTGTCAACTACGAGCGGGCGGCGCGCCCGGCTCTCTGGCGGC 180  
Db 444 GAAGGCACTGTTCAGCGTGTCAACTACGAGCGGGCGGCGCGCCCGGCTCTCTGGCGGC 503  
Qy 181 CTCTGTCTGGGCTTGACAGATATCCACAGGGCGCTGGCGACCTTCGTGTCTGTGTGGC 240  
Db 504 CTCTGTCTGGGCTTGACAGATATCCACAGGGCGCTGGCGACCTTCGTGTCTGTGTGGC 563  
Qy 241 GGCCAGAGCCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTACGGCGGTACGA 300  
Db 564 GGCCAGAGCCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTACGGCGGTACGA 623  
Qy 301 CACATCCCCAGGACAGGTCAGGAGGTCAATGCCAGCATCATCAAAACCCAGAACAC 360  
Db 624 CACATCCCCAGGACAGGTCAGGAGGTCAATGCCAGCATCATCAAAACCCAGAACAC 683  
Qy 361 GTACTGCTGGCTGGTATCCGCTGTGTCAGAGGTCCAGAGGGCGCCGATGGGACGTCGCAAGGC 420  
Db 684 GTACTGCTGGCTGGTATCCGCTGTGTCAGAGGTCCAGAGGGCGCCGATGGGACGTCGCAAGGC 743  
Qy 421 CTTCAAGAGCACGCTCTACTTTGACAGACCTCCAGCGGTACATGCGACAGTTCTGGC 480  
Db 744 CTTCAAGAGCACGCTCTACTTTGACAGACCTCCAGCGGTACATGCGACAGTTCTGGC 803  
Qy 481 TCACCTCGAGGACACCGCGCTGAGGATGCCGTGTCATGAGCAGAGCTCTCCCT 540  
Db 804 TCACCTCGAGGACACCGCGCTGAGGATGCCGTGTCATGAGCAGAGCTCTCCCT 863  
Qy 541 GAATGAGGCGGCTGCTCTGAGGACCTTCCAGAGGTCCGCTGAGTATGGCTGCGTGGT 600  
Db 864 GAATGAGGCGGCTGCTCTGAGGACCTTCCAGAGGTCCGCTGAGTATGGCTGCGTGGT 923  
Qy 601 GCGCATCAGGGGCAAGTCTTCCAGAGGTCCGCGAGGGATCCGAGGCTCCATCTCTC 660  
Db 924 GCGCATCAGGGGCAAGTCTTCCAGAGGTCCGCGAGGGATCCGAGGCTCCATCTCTC 983  
Qy 661 CAGCTGCTCTGACGCTGTGCTACGCGGACATGGAGAACAGTGTTTGGGGGATTCG 720  
Db 984 CAGCTGCTCTGACGCTGTGCTACGCGGACATGGAGAACAGTGTTTGGGGGATTCG 1043  
Qy 721 GCGGACGGGCTGCTCTGAGGATGGTGGATGATTTCTTGGTGACACTCACCTCAC 780  
Db 1044 GCGGACGGGCTGCTCTGAGGATGGTGGATGATTTCTTGGTGACACTCACCTCAC 1103  
Qy 781 CCAGCGGAAACCTTCTCCAGGACCTTCCAGAGGTCCGCTGAGTATGGCTGCGTGGT 840  
Db 1104 CCAGCGGAAACCTTCTCCAGGACCTTCCAGAGGTCCGCTGAGTATGGCTGCGTGGT 1163  
Qy 841 GAACTTCGGAAGACAGTGGTGAACCTTCCCTGTAGAACAGAGGCCCTGGGTGGCAGGC 900  
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Qy 901 T 901  
Db 1224 T 1224

RESULT 2  
US-10-294-778-11  
; Sequence 11, Application US/10294778  
; Publication No. US20030060417A1  
; GENERAL INFORMATION:  
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA  
; TITLE OF INVENTION: No. US20030060417A1e1 Gene Having Reverse Transcriptase Motif  
; FILE REFERENCE: 46124-5034-US  
; CURRENT APPLICATION NUMBER: US/10/294, 778  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US/09/582,924  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: JP 10/13232  
; PRIOR FILING DATE: 1998-01-08

; PRIOR APPLICATION NUMBER: JP 10/33584  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: JP 10/139177  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: PCT/JP99/00039  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 13  
; SEQ ID NO 11  
; LENGTH: 1866  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION:  
US-10-294-778-11

Query Match 100.0%; Score 901; DB 14; Length 1866;  
Best Local Similarity 100.0%; Pred. No. 6e-242;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTCAGACTCCGCTTCATCCCAAGCCTGAGCGGCTGGGCGGATTTGTGAACATGAGACTA 60  
Db 324 GTCAGACTCCGCTTCATCCCAAGCCTGAGCGGCTGGGCGGATTTGTGAACATGAGACTA 383  
Qy 61 CGTCTGGGAGCCAGAACGTTTCCGACAGAAAAAGAGGGCCGAGCGTCTACCTCGAGGGT 120  
Db 384 CGTCTGGGAGCCAGAACGTTTCCGACAGAAAAAGAGGGCCGAGCGTCTACCTCGAGGGT 443  
Qy 121 GAAGGCACTGTTCAGCGTGTCTCAACTACGAGCGGGCGGCGCGCCCGGCTCTCTGGCGGC 180  
Db 444 GAAGGCACTGTTCAGCGTGTCTCAACTACGAGCGGGCGGCGCGCCCGGCTCTCTGGCGGC 503  
Qy 181 CTCTGTCTGGGCTTGACGATATCCACAGGGCTGGCGGACCTTCGTGTCTGTGTGGC 240  
Db 504 CTCTGTCTGGGCTTGACGATATCCACAGGGCTGGCGGACCTTCGTGTCTGTGTGGC 563  
Qy 241 GGCCAGAGCCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGAGGGCGGCTACGA 300  
Db 564 GGCCAGAGCCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGAGGGCGGCTACGA 623  
Qy 301 CACATCCCCAGGACAGGCTTCAGGAGGTCAATGCCAGCATCATCAAAACCCAGAACAC 360  
Db 624 CACATCCCCAGGACAGGCTTCAGGAGGTCAATGCCAGCATCATCAAAACCCAGAACAC 683  
Qy 361 GTACTGCTGGCTGGTATGCCGTGTGTCAGAGGGCGCCGATGGGACGCTCCGCAAGGC 420  
Db 684 GTACTGCTGGCTGGTATGCCGTGTGTCAGAGGGCGCCGATGGGACGCTCCGCAAGGC 743  
Qy 421 CTTCAAGAGCACGCTCTACTTTGACAGACCTCCAGCGGTACATGCGACAGTTCTGGC 480  
Db 744 CTTCAAGAGCACGCTCTACTTTGACAGACCTCCAGCGGTACATGCGACAGTTCTGGC 803  
Qy 481 TCACCTCGAGGACACCGCGCTGAGGATGCCGTGTCATGAGCAGAGCTCTCTCCCT 540  
Db 804 TCACCTCGAGGACACCGCGCTGAGGATGCCGTGTCATGAGCAGAGCTCTCTCCCT 863  
Qy 541 GAATGAGGCGGCTGCTCTGAGGACCTTCCAGAGGTCCGCTGAGTATGGCTGCGTGGT 600  
Db 864 GAATGAGGCGGCTGCTCTGAGGACCTTCCAGAGGTCCGCTGAGTATGGCTGCGTGGT 923  
Qy 601 GCGCATCAGGGGCAAGTCTTCCAGAGGTCCGCGAGGGATCCGAGGCTCCATCTCTC 660  
Db 924 GCGCATCAGGGGCAAGTCTTCCAGAGGTCCGCGAGGGATCCGAGGCTCCATCTCTC 983  
Qy 661 CAGCTGCTCTGACGCTGTGCTACGCGGACATGGAGAACAGTGTTTGGGGGATTCG 720  
Db 984 CAGCTGCTCTGACGCTGTGCTACGCGGACATGGAGAACAGTGTTTGGGGGATTCG 1043  
Qy 721 GCGGACGGGCTGCTCTGAGGATGGTGGATGATTTCTTGGTGACACTCACCTCAC 780  
Db 1044 GCGGACGGGCTGCTCTGAGGATGGTGGATGATTTCTTGGTGACACTCACCTCAC 1103  
Qy 781 CCAGCGGAAACCTTCTCCAGGACCTTCCAGAGGTCCGCTGAGTATGGCTGCGTGGT 840  
Db 1104 CCAGCGGAAACCTTCTCCAGGACCTTCCAGAGGTCCGCTGAGTATGGCTGCGTGGT 1163  
Qy 841 GAACTTCGGAAGACAGTGGTGAACCTTCCCTGTAGAACAGAGGCCCTGGGTGGCAGGC 900  
Db 1164 GAACTTCGGAAGACAGTGGTGAACCTTCCCTGTAGAACAGAGGCCCTGGGTGGCAGGC 1223  
Qy 901 T 901  
Db 1224 T 1224

Db 1104 CCACGGGAAACCTTCTCCAGGACCTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGT 1163  
QY 841 GAACCTGGGAGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGGACGGC 900  
Db 1164 GAACCTGGGAGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGGACGGC 1223  
QY 901 T 901  
Db 1224 T 1224

RESULT 3  
US-09-749-728B-32  
; Sequence 32, Application US/09749728B  
; Patent No. US20020142457A1  
; GENERAL INFORMATION:  
; APPLICANT: Umezawa, Akihiro  
; APPLICANT: Hata, Jun-Ichi  
; APPLICANT: Fukuda, Keiichi  
; APPLICANT: Ogawa, Satoshi  
; APPLICANT: Sakurada, Kazuhiro  
; APPLICANT: Gojo, Satoshi  
; APPLICANT: Yamada, Yoji  
; TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOMYOCYTES  
; FILE REFERENCE: 00766.000043  
; CURRENT APPLICATION NUMBER: US/09/749,728B  
; CURRENT FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: H11-372826  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: PCT-JP00-01148  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: PCT-JP00-07741  
; PRIOR FILING DATE: 2000-11-02  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn Ver.2.0  
; SEQ ID NO 32  
; LENGTH: 3396  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; OTHER INFORMATION: (1)..(3399)  
US-09-749-728B-32

Query Match 100.0%; Score 901; DB 10; Length 3396;  
Best Local Similarity 100.0%; Pred. No. 6.5e-242;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTCCAGACTCCGCTTCATCCCAAGCCTGACCGGCTGGCGCGATTGTGAACATGGACTA 60  
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QY 121 GAAGGACTGTTACGGTCTCACTACGAGGCGGCGCGCGCGCTCCTGGGCGC 180  
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Db 2214 GTACTGCGTGGTGGTATGCCGTGCCAGAAAGCCGCCCATGGGACGCTCCGCAAGGC 2273  
QY 421 CTTCAAGACCCAGCTCTTACCTTGACAGACCTCCAGCGGTACATCGACAGTTCGTGGC 480  
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Db 2334 TCACCTGCAGGAGACACGCGCTGAGGATGCCGTGCTCATCGAGACAGGTTCCTCCCT 2393  
QY 541 GAATGAGGCGACGAGTGGCTCTTCGACGCTTCCTTACGCTTCATCTGCGACACCGCT 600  
Db 2394 GAATGAGGCGACGAGTGGCTCTTCGACGCTTCCTTACGCTTCATCTGCGACACCGCT 2453  
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Db 2514 CACGCTGCTTCGAGGCTGTGTACGGCGACATGGAGAACAGCTGTTTGGCGGGATTGG 2573  
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QY 781 CCACGCGAAACCTTCTCAGGACCTGGTCCGAGGTGTCCTGAGTATGGTGCCTGGT 840  
Db 2634 CCACGCGAAACCTTCTCAGGACCTGGTCCGAGGTGTCCTGAGTATGGTGCCTGGT 2693  
QY 841 GAACCTGGGAGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCGCTGGGTGGCACGGC 900  
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QY 901 T 901  
Db 2754 T 2754

RESULT 4  
US-10-205-629-1  
; Sequence 1, Application US/10205629  
; Publication No. US20030049236A1  
; GENERAL INFORMATION:  
; APPLICANT: Kassem, Moustapha  
; APPLICANT: Jensen, Thomas  
; APPLICANT: Rattan, Suresh  
; TITLE OF INVENTION: Immortalized Stem Cells  
; FILE REFERENCE: 006148.00002  
; CURRENT APPLICATION NUMBER: US/10/205,629  
; PRIOR FILING DATE: 2002-07-26  
; PRIOR APPLICATION NUMBER: 60/315939  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: PA 2001 01148  
; PRIOR FILING DATE: 2001-07-27  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3453  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-205-629-1  
Query Match 100.0%; Score 901; DB 14; Length 3453;  
Best Local Similarity 100.0%; Pred. No. 6.5e-242;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTCCAGACTCCGCTTCATCCCAAGCCTGACCGGCTGGCGCGATTGTGAACATGGACTA 60  
Db 1863 GTCCAGACTCCGCTTCATCCCAAGCCTGACCGGCTGGCGCGATTGTGAACATGGACTA 1922  
QY 61 COTGCTGGGAGCCAGAACCTTCGCGAGAGAAAGAGGCGCGGCTCTCACCTCGAGGTT 120

Db 1923 CGTCGTGGGAGCAGAACTGTCGACAGAAAAGAGGGCGAGCGTCTACCTCGAGGGT 1982  
Qy 121 GAAGGCACTGTTTACGCTGCTCAACTACGAGCGGGCGCGCGCCCGCTCTCTGGCGC 180  
Db 1983 GAAGGCACTGTTTACGCTGCTCAACTACGAGCGGGCGCGCGCCCGCTCTCTGGCGC 2042  
Qy 181 CTCTGTGCTGGGCTGGACGATATCCACAGGGCTGGCGACCTTCGTGTGCTGTGCG 240  
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Qy 241 GGGCAGGACCGCGCTGAGCTGACTTTTCAAGGTGGATGTGAGGGCGGGTACGA 300  
Db 2103 GGGCAGGACCGCGCTGAGCTGACTTTTCAAGGTGGATGTGAGGGCGGGTACGA 2162  
Qy 301 CACCATCCCCCAGGACAGGCTCAGGAGGTCAATCGCCAGCATCATCAAAACCCAGAACAC 360  
Db 2163 CACCATCCCCCAGGACAGGCTCAGGAGGTCAATCGCCAGCATCATCAAAACCCAGAACAC 2222  
Qy 361 GTACTGCGTGGCTGGATGCGGTGTCAGAGGGCGCCCATGGGCACGTCGCAAGGC 420  
Db 2223 GTACTGCGTGGCTGGATGCGGTGTCAGAGGGCGCCCATGGGCACGTCGCAAGGC 2282  
Qy 421 CTTCAAGAGCCAGCTCTTACCTTGACAGACCTCCAGCCGTACATGGGACAGTTCGTGGC 480  
Db 2283 CTTCAAGAGCCAGCTCTTACCTTGACAGACCTCCAGCCGTACATGGGACAGTTCGTGGC 2342  
Qy 481 TCACCTGCAGGACGACAGCGGCTGAGGGATGCGCTCATGAGCAGAGCTCCCTCCCT 540  
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Qy 781 CCACGGGAAACCTTCTCAGGACCTGCTCGAGGCTGCTCCCTGAGTATGGCTGCGTGGT 840  
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Db 2763 T 2763

RESULT 5  
US-09-733-294A-3  
; Sequence 3, Application US/09733294A  
; Patent No. US20020045588A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monla  
; APPLICANT: William Gaarde  
; APPLICANT: Susan M. Freier  
; APPLICANT: Edward V. Wanciewicz  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION  
; FILE REFERENCE: ISPH-0527  
; CURRENT APPLICATION NUMBER: US/09/733,294A  
; CURRENT FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: 09/572,423  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 108  
; SEQ ID NO 3  
; LENGTH: 4015  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (56)....(3454)  
US-09-733-294A-3

Query Match 100.0%; Score 901; DB 9; Length 4015;  
Best Local Similarity 100.0%; Pred. No. 6.6e-242;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTCAGACTCGCTTCATCCCAAGCCTGAGGGCTGGGCCGATGTGAACATGGACTA 60  
Db 1909 GTCAGACTCGCTTCATCCCAAGCCTGAGGGCTGGGCCGATGTGAACATGGACTA 1968  
Qy 61 CGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGCCGAGCGTCTCACCTCGAGGT 120  
Db 1969 CGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGCCGAGCGTCTCACCTCGAGGT 2028  
Qy 121 GAAGGCACTGTTTACGCTGCTCAACTACGAGCGGGCGCGCGCCCGCTCTCTGGCGC 180  
Db 2029 GAAGGCACTGTTTACGCTGCTCAACTACGAGCGGGCGCGCGCCCGCTCTCTGGCGC 2088  
Qy 181 CTCTGTCTGGGCTTGACCATATCCACAGGGCTGGCGACCTTCGTGTGCTGTGGC 240  
Db 2089 CTCTGTCTGGGCTTGACCATATCCACAGGGCTGGCGACCTTCGTGTGCTGTGGC 2148  
Qy 241 GGGCCAGAGCCCGCGCTGAGCTGTACTTTTCAAGTGGATGTGACGGCGGTACGA 300  
Db 2149 GGGCCAGAGCCCGCGCTGAGCTGTACTTTTCAAGTGGATGTGACGGCGGTACGA 2208  
Qy 301 CACCATCCCCCAGGACAGGCTCACGAGGTATCCGCCAGCATCATCAAAACCCAGAACAC 360  
Db 2209 CACCATCCCCCAGGACAGGCTCACGAGGTATCCGCCAGCATCATCAAAACCCAGAACAC 2268  
Qy 361 GTACTGCTGGTGGTATGCCGTGGTCCAGAGGGCGCCCATGGGCACGTCGCCAAGC 420  
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Qy 421 CTTCAAGAGCCAGCTCTTACCTTGACAGACTCCAGCGTACATGGACAGTTCGTGGC 480  
Db 2329 CTTCAAGAGCCAGCTCTTACCTTGACAGACTCCAGCGTACATGGACAGTTCGTGGC 2388  
Qy 481 TCACCTGCAGAGACACGCGCTGAGGGATGCCGTCTCATCAGCAGAGCTCCTCCCT 540  
Db 2389 TCACCTGCAGAGACACGCGCTGAGGGATGCCGTCTCATCAGCAGAGCTCCTCCCT 2448  
Qy 541 GAATGAGGCGAGTGGCTCTTCGACGCTTCCTACGCTTCATGTGCCACACGCGGT 600  
Db 2449 GAATGAGGCGAGTGGCTCTTCGACGCTTCCTACGCTTCATGTGCCACACGCGGT 2508  
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Db 2509 GCGCATCAGGGGCAAGTCCCTACGTCAGTGGCAGGGATCCCGCAGGGCTCCATCCCTC 2568  
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Db 2569 CAGCGTCTTGACGCTGCTGTACGGCAGATGAGGAACAGCTGTTTGGGGGATTCG 2628  
Qy 721 GCGGAGCGGCTGCTCTCGCTGGTGGTGGATGATTTCTTGTGGTACACCTCACCTCAC 780  
Db 2629 GCGGAGCGGCTGCTCTCGCTGGTGGTGGATGATTTCTTGTGGTACACCTCACCTCAC 2688  
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Db 2689 CCACGGGAAACCTTCTCAGGACCTGGTCCGAGGTGCTCCCTGAGTATGGCTGCGTGGT 2748  
Qy 841 GAACCTTGGGAGACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCGCTGGTGGCAGGC 900







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;
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; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 015389-003600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "human telomerase reverse
; transcriptase (hTERT)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-953-052-1

Query Match 100.0%; Score 901; DB 10; Length 4015;
Best Local Similarity 100.0%; Pred. No. 6.6e-242;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGCTGCGCCGATGTGAACATGACTA 60
DB 1909 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGCTGCGCCGATGTGAACATGACTA 1968
QY 61 CGTCGTGGAGCCAGACAGTTCCTCCGAGAGAAAGAGCGCGAGCTCTCACCTCAGGGT 120
DB 1969 CGTCGTGGAGCCAGACAGTTCCTCCGAGAGAAAGAGCGCGAGCTCTCACCTCAGGGT 2028
QY 121 GAAGGACATGTTACGCTGCTCAACTACGAGGGCGCGCGCCCGGCTCTCGGGGCG 180
DB 2029 GAAGGACATGTTACGCTGCTCAACTACGAGGGCGCGCGCCCGGCTCTCGGGGCG 2088
QY 181 CTCTGTGTGGCCCTGGAGGATATCCACAGGCGCTGGCGCACTTCTGCTCGGTGGG 240
DB 2089 CTCTGTGTGGCCCTGGAGGATATCCACAGGCGCTGGCGCACTTCTGCTCGGTGGG 2148
QY 241 GCGCCAGGACCGCGCCCTGAGCTGCTACTTTGTCAAGGTGATGTGACGGCGCGCTACGA 300
DB 2149 GCGCCAGGACCGCGCCCTGAGCTGCTACTTTGTCAAGGTGATGTGACGGCGCGCTACGA 2208
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DB 2209 CACCATCCCGCAGGACAGGCTCACGAGGTATCCGCCAGCATCATCAAAACCCAGAACAC 2268
QY 361 GTACTGCGTGGCTCGGTATCGCGTGTCCAGAGGCGCGCCATGGCGAGCTCCGCAAGGC 420
DB 2269 GTACTGCGTGGCTCGGTATCGCGTGTCCAGAGGCGCGCCATGGCGAGCTCCGCAAGGC 2328
QY 421 CTTCAAGAGCCACGCTCTTACCTTGACAGACCTCCAGCGGTACATCCGACAGTTCGTGGC 480
DB 2329 CTTCAAGAGCCACGCTCTTACCTTGACAGACCTCCAGCGGTACATCCGACAGTTCGTGGC 2388
QY 481 TCACCTGAGGAGACACCGCGCTGAGGATGCCCTGTCTATCGAGCAGAGTCTCTCCCT 540
DB 2389 TCACCTGAGGAGACACCGCGCTGAGGATGCCCTGTCTATCGAGCAGAGTCTCTCCCT 2448
QY 541 GAATGAGCCAGCAGTGGCTCTTCGAGCTCTTCCTAGCTTCATGTCCTCCACAGCGGT 600
DB 2449 GAATGAGCCAGCAGTGGCTCTTCGAGCTCTTCCTAGCTTCATGTCCTCCACAGCGGT 2508
QY 601 GCGCATGAGGGCAAGTCTTACGTCAGTCCAGTGGCGGGATCCGCGAGGGCTCCATCTCTC 660
DB 2509 GCGCATGAGGGCAAGTCTTACGTCAGTCCAGTGGCGGGATCCGCGAGGGCTCCATCTCTC 2568
QY 661 CAGCTGCTCTGACGCCCTGTGCTACGGGACATGAGAACACAGCTGTTTGGGGGATTGG 720
DB 2569 CAGCTGCTCTGACGCCCTGTGCTACGGGACATGAGAACACAGCTGTTTGGGGGATTGG 2628
QY 721 GCGGACGCGGCTGCTCTCGCTTTTGGTGATGATTCTTGTGGTGACACCTCACTCAC 780
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DB 2629 GCGGACGCGGCTGCTCTCGCTTTGTTGGTGATGATTCTTGTGGTGACACCTCACTCAC 2688
QY 781 CCACGCGAAACCTTCTCTCAGGACCTGCTGTCGAGGTGTCCCTGAGTATGGCTGCGTGT 840
DB 2689 CCACGCGAAACCTTCTCTCAGGACCTGCTGTCGAGGTGTCCCTGAGTATGGCTGCGTGT 2748
QY 841 GAACTTGGGAAGACAGTGGTGAACCTTCCCTGTAGAACAGAGGCGCTCGGTGGACGCG 900
DB 2749 GAACTTGGGAAGACAGTGGTGAACCTTCCCTGTAGAACAGAGGCGCTCGGTGGACGCG 2808
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DB 2809 T 2809

RESULT 9
US-10-053-758-224
; Sequence 224, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 224:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
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QY 541 GAATGAGCCAGAGTGGCTCTTCCAGCTCTTCCAGCTTCTCCTACGCTTACGTCCTCCAGCCGCT 600
Db 2449 GAATGAGCCAGAGTGGCTCTTCCAGCTCTTCCAGCTTCTCCTACGCTTACGTCCTCCAGCCGCT 2508
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QY 661 CAGCTGCTCTGACGCTGTGTAGCGGACATGGAGAACAGCTGTTTGGCGGGATTCG 720
Db 2569 CAGCTGCTCTGACGCTGTGTAGCGGACATGGAGAACAGCTGTTTGGCGGGATTCG 2628
QY 721 GCGGACAGGGCTCTCTCGTTTGGTGGATGATTTCTTGGTGGACACCTCAGCTCAG 780
Db 2629 GCGGACAGGGCTCTCTCGTTTGGTGGATGATTTCTTGGTGGACACCTCAGCTCAG 2688
QY 781 CCACGCGAAACCTTCTCAGGACCTGTGTCAGGAGTGTCCCTGAGTATGGCTGCTGT 840
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QY 841 GAATGCGGAGACAGTGGTGAATTCCTGTAGAGACAGAGGCGCTGGGTGGACAGCG 900
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Db 2809 T 2809

RESULT 11
US-10-054-295-224
; Sequence 224, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 224:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "hTERT"
; /note= "human telomerase reverse
; transcriptase (hTERT) catalytic protein
; component"
; SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-054-295-224

Query Match 100.0%; Score 901; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 6.6e-242;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGGACTA 60
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QY 61 CGTGTGGGAGCCAGAACGTTCCGAGAGAAAGAGGGCCGAGCGCTCTCACCTCGAGGGT 120
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QY 181 CTCTGTGCTGGGCTGCGAGCATATCCACAGGGGCTGCGCACCTTCTGTGCTGTGGC 240
Db 2089 CTCTGTGCTGGGCTGCGAGCATATCCACAGGGGCTGCGCACCTTCTGTGCTGTGGC 2148
QY 241 GGCCAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGA 300
Db 2149 GGCCAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGA 2208
QY 301 CACCATCCCGCAGGACAGGCTCAGGAGGTCTACGCGAGCATCATCAAAACCCAGAACAC 360
Db 2209 CACCATCCCGCAGGACAGGCTCAGGAGGTCTACGCGAGCATCATCAAAACCCAGAACAC 2268
QY 361 GTACTGCTGCTGCGGTATGCCGTGTCAGAGAGCGCCCATGGGCGACGTCGCCAAGGC 420
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Db 2389 TCACCTGCGAGGAGACCGCCGCTGAGGATGCCGTGCTCATCGACAGAGTCTCCCT 2448
QY 541 GAATGAGCCAGCAGTGGCTCTTCCAGCTTCTTCTACGCTTCTATGTGCCACACCGCGT 600
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QY 601 GCGCATCAGGGCAAGTCTTACCTGACAGGATCCCGCAGGGGATCCCGCAGGGCTCCATCTC 660
Db 2509 GCGCATCAGGGCAAGTCTTACCTGACAGGATCCCGCAGGGGATCCCGCAGGGCTCCATCTC 2568
QY 661 CAGCTGCTCTGACGCTGTGTAGCGGACATGGAGAACAGCTGTTTGGCGGGATTCG 720
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Db 2629 GCGGAGCGGCTGCTCTGCTTGGTGGATGATTTCTTGTGGTACACTCACCTCAC 2688  
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Db 2749 GAACCTCGGGAAGACAGTGTGTAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGSCACGGC 2808  
QY 901 T 901  
Db 2809 T 2809

RESULT 12

US-10-054-611-224  
; Sequence 224, Application US/10054611  
; Publication No. US20030059787A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. US20030059787A1el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/054,611  
; FILING DATE: 18-Jan-2002  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/854,050  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 224:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4015 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 56..3454  
; OTHER INFORMATION: /product= "hTERT"

; /note= "human telomerase reverse  
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; component"  
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Best Local Similarity 100.0%; Pred. No. 6.6e-242;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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; Publication No. US20030068818A1  
; GENERAL INFORMATION:  
; APPLICANT: Geron Corporation  
; APPLICANT: Denning, Chris  
; APPLICANT: Clark, A. John  
; APPLICANT: Schiff, J. Michael  
; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human  
; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System  
; TITLE OF INVENTION: Recombination  
; FILE REFERENCE: 731/002  
; CURRENT APPLICATION NUMBER: US/10/105,963  
; CURRENT FILING DATE: 2002-03-21  
; PRIOR FILING DATE: 2002-03-21  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 4015  
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; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
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; OTHER INFORMATION:  
US-10-105-963-1

Query Match 100.0%; Score 901; DB 14; Length 4015;  
Best Local Similarity 100.0%; Pred. No. 6.6e-242;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 541 GAATGAGGCGCAGCTGGCTCTTCGACGTCTTCCTACGCTTCATGTGCCACACCGCGT 600

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; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND  
; THERAPEUTIC METHODS  
; NUMBER OF SEQUENCES: 335  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
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; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
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; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.

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TOPOLOGY: linear  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	6057	99.6	4015	4	US-09-430-323-224
5	6057	99.6	4015	4	US-09-572-4238-3
6	6057	99.6	4015	4	US-09-128-354-1
7	6057	99.6	4015	4	US-09-675-321-1
8	6057	99.6	4015	4	US-08-912-951-1
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19	5689.5	93.6	3855	4	US-08-974-549A-722	Sequence 722, App
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ALIGNMENTS

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; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Marin, Gregg B.  
; APPLICANT: Haxley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: No. 6093809el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release v1.0, Version #1.30  
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; FILING DATE: 06-MAY-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419

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; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 224:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; NAME/KEY: CDS
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; OTHER INFORMATION: transcriptase (hTERT) catalytic protein
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Db 422 CTGCCAACACGGTGACCGACGCACTGGGGGAGCGGGCGTGGGGGCTGTGCTGCTGCC 481
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QY	545	SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLeuAla	564
DB	1622	AGCCAGGGGTGGCTGTGTCCGGCCGCGAGACCGCTGTGGTGAGGAGATCTGGCC	1681
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QY	585	ValThrGluThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer	604
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QY	605	LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer	624
DB	1802	AAGTTGCAAGCATTTGAAGTACAGACACACTTGAAGAGGTGCAGCTCGCGGAGCTGTCG	1861
QY	625	GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg	644
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QY	645	PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla	664
DB	1922	TTTCATCCCAAGCCTGACGGGCTCGGCCCATTTGAACTGAGTACGTACGTCTGGGAGCC	1981
QY	665	ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe	684
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DB	2042	AGCGTGTCAACTACGAGCGGGCGCGCCCGCCCTCTCTGGCGGCTCTGTGCTGGGC	2101
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QY	765	ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis	784
DB	2282	CGGTATCCGTGTGTCCAGAAGCGGCCCATCGGCGAGCTCGCGAAGGCTTCAAGAGCCAC	2341
QY	785	ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu	804
DB	2342	GTCTCTACCTTGACAGACCTCCAGCGGTACATCGGACAGTTCTGTGCTCAGCTGCAGGAG	2401
QY	805	ThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGluAlaSer	824
DB	2402	ACCAGCCGCTGAGGGATGCCGCTCATCGACGAGCTCCCTCCCTGAATGAGGCCAGC	2461
QY	825	SerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIleArgGly	844
DB	2462	AGTGGCCCTTCACGCTTTCTTCACTACGCTTCATGTGCCACACACCGCTGGCGCATCGGGC	2521
QY	845	LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys	864
DB	2522	AAGTCTTACGTCAGTGCCAGGGGATCCCGAGGGGTCCATCTCTCCAGCTGTCTCTGC	2581
QY	865	SerLeuCystTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu	884
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Db	2702	TTCTCTCAGGACCCCTGGGCTCCGAGGTGTCCTCTAGTATGGCTGCGTGGTGAACCTTGC	2761
QY	925	ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet	944
Db	2762	ACAGTGGTGAACCTTCCCTGTAGAAAGCAGGCCCTGGGTGGCGACGGCTTTGTTCACATG	2821
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Db	2822	CCGCGCCACCGGCCATTCCCTGGTGGCGCTGCTGGATACCCGGACCCCTGGAGGTG	2881
QY	965	GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg	984
Db	2882	CAGAGCAGCTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGCTCTCAGCTTCAACCGC	2941
QY	985	GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys	1004
Db	2942	GGCTTCAAGGCTGGAGGAAACATCGCTCGCAACATCTTTGGGGTCTTTGGCGCTGAAGTGT	3001
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Db	3002	CACAGCCTGTTTCTGGATTTCAGGTGAACAGCCCTCCAGAGCGGTGTCACCCACATCTAC	3061
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Db	3062	AAGATCTCTCTGCTGTCAGGCGTACAGCTTTCACGCATGTGTGTCAGCTCCCATTTTCAT	3121
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QY	1085	GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeu	1104
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QY	1105	ThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGln	1124
Db	3302	ACTCGACACCGGTGTACCTACGTGCCACTCTTGGGGTCACTTCAGGACAGGCCACAGCGAG	3361
QY	1125	LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsnProAla	1144
Db	3362	CTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCTCTGGGCGCGCGACCAACCCGCGCA	3421
QY	1145	LeuProSerAspPheLysThrIleLeuAsp	1154
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## RESULT 2

US-08-974-549A-1-  
; Sequence 1, Application US/08974549A

Patent No. 6166178  
GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin B.  
APPLICANT: Andrews, William H.

; M. LEACHMAN, ANDREWS, WILLIAM H.  
 ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
 ; NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-0026100S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
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OTHER INFORMATION: transcriptase (hTERT) catalytic protein
OTHER INFORMATION: component"
US-08-974-549A-1

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Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	99.64%
DB:	3
	Length:
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	Mismatches:
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US-08-951-733-20 (1-1154) x US-08-974-549A-1 (1-4015)

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Db	1142	ACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTGGCCCGCCTG	1201
QY	405	ProGlnArgTyrTrpGlnMetArgProLeuPheLeuLeuLeuGlyAsnHisAlaGln	424
Db	1202	CCCCAGCGTACTGGCAATATGGGCCCTGTCTTGAGCTGTTGGGAACACGCGCAG	1261
QY	425	CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla	444
Db	1262	TGCCCTACGGGTGCTCTCAAGACGCACTGCCCGCTCGAGCTCGGFTCACCCAGCA	1321
QY	445	AlaGlyValCysAlaArgGlnLysProGlnGlySerValAlaAlaProGlnGluAsp	464
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Db	1442	GGCTTCGTGGGCGCTGCCTGCGCGCTGGTCCCGCCAGGCCCTCGGGCTCCAGGCAC	1501
QY	505	AsnGluArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys	524
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Db	1682	AGTTCTCTGCACGTGGTGTAGTGTGTACGTCTCGTCTGAGCTGCTCAGGCTCTTTCTTTAT	1741
QY	585	ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer	604
Db	1742	GTCCCGGAGACACGTTTCAAGAAGACAGGCTCTTTTCTACCGAAGAGTGTCTGGAGC	1801
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Db	1802	AAGTTCAAGCATTTGGAATCACACAGCACTTTGAAGAGGTGCAGCTGCGGGAGCTGTCG	1861
QY	625	GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg	644
Db	1862	GAAGCAGAGGTCAAGCAGCATCGGAAGCCAGCGCCCGCTGTCAGCTCCAGACTCCGC	1921
QY	645	PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla	664
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Db	2102	CTGGAGATATCCACAGGGCGCTGGCGACCTTCGTGCTGGTGTGGCGCCAGGACCCG	2161
QY	725	ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln	744
Db	2162	CCGCTGTAGCTGTACTTTGTCAAGTGGATGTGACGGGCGGTACACACCATCCCCCAG	2221
QY	745	AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg	764
Db	2222	GACAGGCTCACGAGGTCTATCGCCAGCATCAAAACCCAGAACACGTACTCGTGGCT	2281
QY	765	ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis	784
Db	2282	CGGTATGCGGTGTCCAGAGGCCGCCCATGGCAGCTCCGCAAGGCTTCAAGAGCCAC	2341
QY	785	ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu	804
Db	2342	GTCTCTACCTTTGACAGACCTCCAGCGGTACATCGCAGTTCTGTGGCTCACCTGCAGGAG	2401
QY	805	ThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuLeuAsnGluAlaSer	824
Db	2402	ACCAGCCCGCTGAGGATGCCGTGTCATCGACGAGAGCTCTCCCTGAATGAGGCCAGC	2461
QY	825	SerGlyLeuPheAspValPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu	844
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Db	2642	CTCCTCGTGTGGTGATGATTTCTTGTGTGACACCTCACCTCACCCACGCGAAACCC	2701
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Db	2702	TTCTCAGGACCTGTGTCCGAGGTGTCCTGTAGTATGGCTGCTGGTGAACCTTGGCGAAG	2761
QY	925	ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet	944
Db	2762	ACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCGCTTGGTGGCACGGCTTTTGTTCAGATG	2821
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Db	2822	CCGGCCCCCGCCCTATTCCTCGTGGGCGCTGCTGTGTGATACCCGCGACCTTGGAGGTG	2881
QY	965	GlnSerAspTyrSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg	984
Db	2882	CAGAGCGACTACTCCAGCTATGCCGACCTCCATCAGAGCCAGTCTCACCTTCAACCCG	2941
QY	985	GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys	1004
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QY	1005	HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr	1024
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QY	1025	LysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis	1044
Db	3062	AAGATCTCTCTGTCAGGCGTACAGGTTTTCACGCATGTGTGTGTCAGCTCCCATTTTCAT	3121
QY	1045	GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu	1064
Db	3122	CAGCAAGTTTGGGAAGAACCCACATTTTCTCGCGCTCATCTCTGACAGGGCTCCCTC	3181
QY	1065	CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla	1084
Db	3182	TGCTACTCTCATCTGAAGCCAGAACGAGGATGTGCTGGGGGCCAAGGGCGCGGCC	3241
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## RESULT 3

US-08-854-050-224  
; Sequence 224, Application US/08854050  
; Patent No. 6261836

## GENERAL INFORMATION:

APPLICANT: Tech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: NO.6261836el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,050  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 536

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/951,843  
FILING DATE: 06-MAY-1997  
CLASSIFICATION: 536

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 536

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION: 536

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION: 536

## ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

## INFORMATION FOR SEQ ID NO: 224:

SEQUENCE CHARACTERISTICS:  
LENGTH: 4015 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
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; NAME/KEY: CDS  
; LOCATION: 56...3454  
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; OTHER INFORMATION: /note= "human telomerase reverse  
; transcriptase (hrrt) catalytic protein  
; OTHER INFORMATION: component"  
; US-08-854-050-224

## Alignment Scores:

Pred. No.: 0 Length: 4015  
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Percent Similarity: 100.00% Conservative: 0  
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US-08-951-733-20 (1-1154) x US-08-854-050-224 (1-4015)

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Db	962	CACCAAGCGGGCCGCCATCCATCGCGGCCACACAGTCCCTGGGACACGCTTGTCC	1021	Db	2042	ACGCTGCTCAACTACGAGGCGCGCGCGCTCTCTGGCGCCTCTGTGCTGGCG	2101
QY	345	ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluLeuArg	364	QY	705	LeuAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro	724
Db	1022	CGGGTACGCCAGACCAAGCACCTTCCTACTCTCAGGCGACAAAGAGCAGTGGCG	1081	Db	2102	CTGGAGATATCCACAGGGCTGGCGACCTTCGTGCTGGGTGGCGGCCAGGACCG	2161
QY	365	ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu	384	QY	725	ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln	744
Db	1082	CCCTCCTCTACTCAGCTCTCTGAGGCCACGCTGACTGGCTCGGAGGCTCGTGGAG	1141	Db	2162	CGGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGCGGTACGACACCATCCCCAG	2221
QY	385	ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu	404	QY	745	AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg	764
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Db	1862	GAAGCAGAGTTCAGGCAGCATCGGGAAGCCAGCGCGCCTGTGTACGTCCAGACTCCGC	1921	Db	2942	GGCTTCAAGGCTGGGAGAACATCGCTCGCAAACTCTTTGGGCTCTTTCGCGCTGAAGTGT	3001
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RESULT 4

US-09-430-323-224  
: Sequence 224, Application US/09430323  
: Patent No. 6309867  
: GENERAL INFORMATION:  
: APPLICANT: Cech, Thomas R.  
: Lingner, Joachim  
: Nakamura, Toru  
: Chapman, Karen B.  
: Morin, Gregg B.  
: Harley, Calvin  
: Andrews, William H.  
: TITLE OF INVENTION: No. 6309867el Telomerase  
: NUMBER OF SEQUENCES: 225  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Townsend and Townsend and Crew LLP  
: STREET: Two Embarcadero Center, 8th Floor  
: CITY: San Francisco  
: STATE: California  
: COUNTRY: United States of America  
: ZIP: 94111  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: FILING APPLICATION NUMBER: US/09/430,323  
: FILING DATE: 29-Oct-1999  
: CLASSIFICATION: <Unknown>  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/854,050  
: FILING DATE: 09-MAY-1997  
: APPLICATION NUMBER: US 08/851,843  
: FILING DATE: 06-MAY-1997  
: APPLICATION NUMBER: US 08/846,017  
: FILING DATE: 25-APR-1997  
: APPLICATION NUMBER: US 08/844,419  
: FILING DATE: 18-APR-1997  
: APPLICATION NUMBER: US 08/724,643  
: FILING DATE: 01-OCT-1996  
: ATTORNEY/AGENT INFORMATION:

: NAME: Apple, Randolph T.  
: REGISTRATION NUMBER: 36,429  
: REFERENCE/DOCKET NUMBER: 015389-002930US  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (415) 576-0200  
: TELEFAX: (415) 576-0300  
: INFORMATION FOR SEQ ID NO: 224:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 4015 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: cdna  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: 56..3454  
: OTHER INFORMATION: /product= "hTERT"  
: /note= "human telomerase reverse  
: transcriptase (hTERT) catalytic protein  
: component"  
: SEQUENCE DESCRIPTION: SEQ ID NO: 224:  
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Alignment Scores:  
Pred. No.: 0 Length: 4015  
Score: 6057.00 Matches: 1150  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.64% Indels: 0  
DB: 4 Gaps: 0  
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Db 2 CAGCGCTGCGTCTGCTGCGCACGTGGGAAGCCCTGGCCCGCGGCACCCCGCGATGCCG 61  
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Db 122 CCGCTGGCCACGTTTCGTGCGCGCTGCGGCCCGCCAGGCGCTGGCGCTGGTGCACGCGGG 181  
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QY	225	TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg	244		Db
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QY	265	AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr	284		Db
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QY	285	ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla	304		Db
Db	842	CGTGACCGAGTACCGTGTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	901		QY
QY	305	ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln	324		Db
Db	902	ACCTCTTTGGAGGGTGCCTCTCTGTGCACGCGCCACTCCACCCATCCGTGGCGCCGAG	961		QY
QY	325	HisHisAlaGlyProProSerThrSerArgProProArgProTrpArgThrProCysPro	344		Db
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QY	345	ProValTrpAlaGluThrLysHisPheLeuTrpSerSerGlyAspLysGlnLeuArg	364		Db
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QY	365	ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu	384		Db
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Db	1262	TGCCCCCTACGGGGTGTCTCTAAGACGCACTCCCGCTGCGAGCTGCGGTCAACCGACA	1321		QY
QY	445	AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp	464		Db
Db	1322	GCCGTGTCTGTGCGCGGAGAGCCCGCAGGGCTCTGTGGCGGCCCGCGAGGAGGAGAC	1381		QY
Db	465	ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr	484		Db
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QY	565	LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyr	584		Db
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Db	585	ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer	604		Db
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Qy 1005 HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr 1024
Db 3002 CACAGCCTGTTTCTGGATTTCAGGTGAACAGCCTCCAGAGGTGTGCACCAACATCTAC 3061
Qy 1025 LysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis 1044
Db 3062 AAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCAATGTGTGTGCAGCTCCCATTTTCAT 3121
Qy 1045 GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu 1064
Db 3122 CAGCAAGTTTGGAGAACCCACCATTTTCTGCGCGTCACTCTGACAGGCGCTCCCTC 3181
Qy 1065 CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla 1084
Db 3182 TGTACTTCCATCTCTGAAAGCGCAAGACGAGGATGTCTGTGGGGGCCAAGGGCGCGCC 3241
Qy 1085 GlyProLeuProSerGluAlaValGlnTrpLeuGlySerLeuAlaPheLeuLysLeu 1104
Db 3242 GGCCCTCTGCCCTCCGAGGCGGTGACGTGCTGTGCCAACCAAGCATTTCTTGTCAAGCTG 3301
Qy 1105 ThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGln 1124
Db 3302 ACTCGACACGGTGCACCTACGTGGCCACTCTTGGGGTCACTCAGGACAGCCAGACCCAG 3361
Qy 1125 LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsnProAla 1144
Db 3362 CTGAGTCGGAAGCTCCCGGGGAGACGCTGACTGCCCTGGAGGCCGCGAGCAACCCGGCA 3421
Qy 1145 LeuProSerAspPheLysThrIleLeuAsp 1154
Db 3422 CTGCCCTCAGACTTCAAGACCATCTCTGGAC 3451
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## RESULT 5

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US-09-572-423B-3
; Sequence 3, Application US/09572423B
; Patent No. 6331399
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William A. Gaarde
; APPLICANT: Edward Wancewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0462
; CURRENT APPLICATION NUMBER: US/09/572,423B
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)...(3454)
US-09-572-423B-3
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## Alignment Scores:

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Pred. No.: 0 Length: 4015
Score: 6057.00 Matches: 1150
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Query Match: 99.64% Indels: 0
DB: 4 Gaps: 0
US-08-951-733-20 (1-1154) x US-09-572-423B-3 (1-4015)

Qy 5 GlnArgCysValLeuLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro 24
Db 2 CAGCGCTGCGTCTCTGCTGCGCACGTGGGAAGCCCTGGCCCGGCACCCCGCGATCGCG 61
Qy 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44
Db 62 CGCGCTCCCGCTGCGGAGCGGTGCGTCTGCTGCGACGCCACTACCGCGAGGTGCTG 121
Qy 45 ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64
Db 122 CCGCTGCCACGTTCGTGCGCGCGCTGGGGCCCCAGGCTGGCGCTGGTGGCGGCGG 181
Qy 65 AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla 84
Db 182 GACCGCGCGCTTTCCGCGCGCTGTGTGGCCAGTGCCTGGTGTGCTGCGCTGGGAGCA 241
Qy 85 ArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104
Db 242 CGGCGCGCCCCCGCGCGCCCCCTCTCCGCGAGGTGCTGCTGCTGAAGGAGCTGGTGCC 301
Qy 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124
Db 302 CGAGTGTCTCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCTTCGGCTTCGCG 361
Qy 125 LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr 144
Db 362 CTGTGTGACGGGGCGCGGGGGCCCCCGGAGGCTTCACACAGCGTGCAGAGTAC 421
Qy 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuArg 164
Db 422 CTGCCCCAACCGGTGACCGCGCACTGCGGGGGAGCGGGGCTGGGGCTGCTGCTGCGC 481
Qy 165 ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal 184
Db 482 CGCGTGGCGACGACGCTGCTGGTTCACTGCTGGCACGCTGCGCGCTCTTTGTGCTGCTG 541
Qy 185 AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr 204
Db 542 GCTCCAGCTGCGCTTACCAGGTGTGCGGGCGCGCGCTGTACACAGCTGCGCGCTGCCACT 601
Qy 205 GlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGluArgAla 224
Db 602 CAGCGCGCGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGCGCC 661
Qy 225 TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg 244
Db 662 TGGAAACCATAGCGTCAGGAGCGCGGGTCCCGCTGGGCGCTGCCAGCCCGGGTGGAGG 721
Qy 245 ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla 264
Db 722 AGGCGGGGGGAGTGCAGCCGAAGTCTGCGGTGCCCAGAGGCCAGCGCGTGGGCGCT 781
Qy 265 AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr 284
Db 782 GCCCTTGAGCGGAGCGGACGCCCGTTGGCAGGGGTCTTGGGCCCCACCCGGGCGAGCG 841
Qy 285 ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluGluAla 304
Db 842 CGTGGACCGAGTGACCGTGGTCTTCTGTGTGTGTGTCAGCTGCGACAGCCCGCGGAAGACC 901
Qy 305 ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln 324
Db 902 ACCTCTTGGAGGGTGCCTCTCTGGCACGCGGCCACTCCCAACCATCTCGTGGGCGCGCAG 961
Qy 325 HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro 344
Db 962 CACCACGGGGCCCCCATCCACATCGGGGCCACCATGCTCCCTGGGACACGCGCTTGTCCTC 1021
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QY	345	ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluInLeuArg	364	
Db	1022	CCGGTGACCCGAGACCAAGCACTTCTCTACTCTCAGGCACAGAGACAGCTGCGG	1081	
QY	365	ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgLeuValGlu	384	
Db	1082	CCCTCCTCTCTACTCAGCTCTCTGAGGCCAGCAGCTGACTGGCGCTCGGAGCTCGTGAG	1141	
QY	385	ThrIlePheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuProArgLeu	404	
Db	1142	ACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGACCTCCCGCAGGTTGCCCGCCCTG	1201	
QY	405	ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln	424	
Db	1202	CCCCAGCGCTACTGGCAATGCGGCCCTGTTCTGGAGCTGTTGGGAACACAGCGCAC	1261	
QY	425	CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla	444	
Db	1262	TGCCCCCTACGGGTGCTCTCAAGACGCACTGCCCGCTCGAGCTGCGGTCACCCCAGCA	1321	
QY	445	AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAAsp	464	
Db	1322	GCCGGTGTCTGTCCCGGGAGAACCCCAAGGGCTCTGTGGCGGCCCCCGAGGAGGAGAC	1381	
QY	465	ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr	484	
Db	1382	ACAGACCCCGCTGCTGGTGACGTGCTCCGCGCACACAGACGCCCTGGCAGGTGTAC	1441	
QY	485	GlyPheValArgAlaCysLeuArgArgLeuValProGlyLeuTrpGlySerArgHis	504	
Db	1442	GGCTTCGTGGGGCTTCCTGCGCGCTGCTGCCCGCCAGCGCTCTGGGGCTCCAGGCAC	1501	
QY	505	AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys	524	
Db	1502	AAGCAAGCGCTCTCTCAGGAACCAAGAAGTTCTCTCCCTGGGGAAGCATGCCAAG	1561	
QY	525	LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg	544	
Db	1562	CTCTCGCTCAGGAGCTGACGTGGAGATGAGCGTGGGAGCTGCGCTGGCTGCCGAGG	1621	
QY	545	SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLeuAla	564	
Db	1622	AGCCAGGGGTTGGCTGTGTTCGGCGCGCAGACACCGCTGCGTGAGGAGATCTTGGCC	1681	
QY	565	LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPheTyr	584	
Db	1682	AAGTTCCTGACGTGGCTGATGATGTAGTGTAGCTGCTCAGCTGCTCAGGTCTTCTTTAT	1741	
QY	585	ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer	604	
Db	1742	GTACCGAGACACCGTTTCAAAAGACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGC	1801	
QY	605	LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgLeuSer	624	
Db	1802	AAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGGGGAGCTGTGC	1861	
QY	625	GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg	644	
Db	1862	GAGCAGAGGTACAGCAGCATCGGAAGCCAGGCGCCCTGCTCAGCTCCAGACTCCGC	1921	
QY	645	PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla	664	
Db	1922	TTCATCCCAAGCCTCAGCGGCTGCGCGGATGTGAACATGACGTACGTCGTGGAGCC	1981	
QY	665	ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe	684	
Db	1982	AGAACTTCGCGAGAAAAAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACGTTC	2041	
QY	685	SerValLeuAsnTyrGluArgAlaArgProGlyLeuLeuGlyAlaSerValLeuGly	704	
Db	2042	AGCGTCTCAACTACAGCGGGCGCGCGCCCTCTCGGGCCCTCTGTGCTGGCC	2101	
QY	705	LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro	724	
Db	2102	CTGGCAGATATCCACAGGGCTGGCGCACCTTGTGCTGCTGTGGGGCCAGGACCCG	2161	
QY	725	ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln	744	
Db	2162	CCGCCCTGAGCTGTACTTGTCAAGTGGATGTACGGGCGGTACGACACCATCCCCCAG	2221	
QY	745	AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg	764	
Db	2222	GACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGAACAGTACTGCGTGGT	2281	
QY	765	ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis	784	
Db	2282	CGGTATGCCGTGTTCAGAAAGCGCCCATGGGCATGCGCAAGGCTTCAGAGGCCAC	2341	
QY	785	ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu	804	
Db	2342	GTCTCTACCTTGACAGACCTCCAGCGCTACATGCGACAGTTCGTGGGTCACTGCAGGAG	2401	
QY	805	ThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGluAlaSer	824	
Db	2402	ACCAGGCCGCTGAGGGATCGCTGTCATCGACGAGAGCTCTCCCTGAAATGAGGCCAGC	2461	
QY	825	SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly	844	
Db	2462	AGTGGCTCTTCCAGCTTCTTCTACGCTTCTATGTCACACCGCGGTGCCATCAGGGGC	2521	
QY	845	LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys	864	
Db	2522	AAGTCTCATGCTCCAGTGCCAGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTGC	2581	
QY	865	SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu	884	
Db	2582	AGCTGTGCTACGGCGACATGGAGAACAGCTTTTTCGGGGATTCGGCGGGAGCGGCTG	2641	
QY	885	LeuLeuArgLeuValAspAspPheLeuValThrProHisLeuThrHisAlaLysThr	904	
Db	2642	CTCTCGGTTTGGTGGATGATTTCTTGTGCTGACACCTCACCTCACCGCGGAAACCC	2701	
QY	905	PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys	924	
Db	2702	TTCTCTCAGGACCTGGTCCGAGGTGTCCTTGAGTATGGCTGCGTGGTGAACCTTGGCAGG	2761	
QY	925	ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet	944	
Db	2762	ACAGTGGTGAACTTCCCTGTAGAGAGCAGGCGCTTGGGTGGCAGCGCTTTGTTCAGATG	2821	
QY	945	ProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeuGluVal	964	
Db	2822	CCGGCCACGGCCTATTCCCTGCTGGCGGCTGCTGCTGGATACCGGACCTTGGAGGTG	2881	
QY	965	GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg	984	
Db	2882	CAGAGGACTACTTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCCG	2941	
QY	985	GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys	1004	
Db	2942	GGCTTCAAGGCTGGGAGAACATGCGTCGCAAACTCTTTGGGGTCTTGGCGCTGAAGTGT	3001	
QY	1005	HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr	1024	
Db	3002	CACAGCCTGTTCTTGGATTTGCAAGTTCAGAGCCTCCAGAGCGTGTGCACCAACATCTAC	3061	
QY	1025	LysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis	1044	
Db	3062	AAGATCTCTCTGTCAGGCGTACAGGTTTTCAGGCATGTGTGTCAGCTGCCATTTTCAT	3121	
QY	1045	GlnGluValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu	1064	
Db	3122	CAGCAAGTTTGAAGAACCCACATTTTCTCGCGTCACTCTGTGACAGGGCTCCCTC	3181	
QY	1065	CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla	1084	

Db 3182 TGCTACTCCATCCTCAAGGCCAAGACCCAGGATGTGCTGGGGGCCAAGGGCCGCC 3241  
QY 1085 GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeu 1104  
Db 3242 GGCCTCTGCCCTCCGAGGGCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTG 3301  
QY 1105 ThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGln 1124  
Db 3302 ACTCGACACCGGTGCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAGACGCG 3361  
QY 1125 LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsnProAla 1144  
Db 3362 CTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCTGGAGCGCGAGCCAAACCGGCA 3421  
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RESULT 6  
US-09-128-354-1  
; Sequence 1, Application US/09128354  
; Patent No. 6337200  
; GENERAL INFORMATION:  
; APPLICANT: Morin, Gregg B.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants  
; FILE REFERENCE: 015389-003310US  
; CURRENT APPLICATION NUMBER: US/09/128,354  
; EARLIER FILING DATE: 1998-08-03  
; EARLIER APPLICATION NUMBER: US 08/851,843  
; EARLIER FILING DATE: 1997-05-06  
; EARLIER APPLICATION NUMBER: US 08/854,050  
; EARLIER FILING DATE: 1997-03-09  
; EARLIER APPLICATION NUMBER: US 08/911,312  
; EARLIER FILING DATE: 1997-08-14  
; EARLIER APPLICATION NUMBER: US 08/912,951  
; EARLIER FILING DATE: 1997-08-14  
; EARLIER APPLICATION NUMBER: US 08/915,503  
; EARLIER FILING DATE: 1997-08-14  
; EARLIER APPLICATION NUMBER: WO PCT/US97/17618  
; EARLIER FILING DATE: 1997-10-01  
; EARLIER APPLICATION NUMBER: WO PCT/US97/17885  
; EARLIER FILING DATE: 1997-10-01  
; EARLIER APPLICATION NUMBER: US 08/974,549  
; EARLIER FILING DATE: 1997-11-19  
; EARLIER APPLICATION NUMBER: US 08/974,584  
; EARLIER FILING DATE: 1997-11-19  
; EARLIER APPLICATION NUMBER: US 09/052,864  
; EARLIER FILING DATE: 1998-03-31  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4015  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (56)..(3454)  
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA  
US-09-128-354-1

Alignment Scores:  
Pred. No.: 0 Length: 4015  
Score: 6057.00 Matches: 1150  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.64% Indels: 0  
DB: 4 Gaps: 0

US-08-951-733-20 (1-1154) x US-09-128-354-1 (1-4015)

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Db 2 CAGCGCTCGGCTCTGCTGGCGACGFTGGGAAGCCCTGGCCCGCGCACCCGCCGATGCGG 61  
QY 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44  
Db 62 CGCGCTCCCGCTGCCGAGCGTGGCTCTCTGCTGCCAGCCACTACCGGAGGTGCTG 121  
QY 45 ProLeuAlaThrPheValArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64  
Db 122 CCGCTGGCACGTTCTGTCGGCGCTGGGGCCCCAGGCTGGCGCTGGTGGCGCGG 181  
QY 65 AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla 84  
Db 182 GACCGGGGGCTTTCGGCGCTGTGTGGCCAGTGCCTGGTGGTGGCTGGCGACGCA 241  
QY 85 ArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104  
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Db 362 CTGCTGGACGGGGCGCGGGGGCGCGCGCGCTTCACCAACAGCGTGCAGCTGCGAGTAC 421  
QY 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeuLeuArg 164  
Db 422 CTGCCCAACACGGTGCACGACGCTGGGGGGAGCGGGGGTGGGGCTGCTGGTGGCG 481  
QY 165 ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal 184  
Db 482 CGCGTGGCGACGACGCTGCTGTTTCACTGTGGCGACGCTGCGCGCTCTTTTGTGGTG 541  
QY 185 AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr 204  
Db 542 GCTCCAGCTCGGCTACCAAGTGTGGGGCGCGCGCTGTACCAAGCTGCGGCGTGCCTACT 601  
QY 205 GlnAlaArgProProHisAlaSerGlyProArgArgLeuGlyCysGluArgAla 224  
Db 602 CAGCGCGCGCGCGCGCGCTAGTGGACCCCGAAGCGCTCTGGGATGCGAAGCGGCC 661  
QY 225 TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg 244  
Db 662 TGAACCATAGCTCAGGAGCGCGGGTCCCTTGGGCTTGCAGCCCGCGGTCGCGAGG 721  
QY 245 ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysAlaGProArgArgGlyAla 264  
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QY 265 AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr 284  
Db 782 GCCCTGAGCGGAGCGGACGCCCTTGGGCGAGGGTCTCTGGGCGCGCGCGCGGCGAGG 841  
QY 285 ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla 304  
Db 842 CGTGGACCGAGTACCGTGGTTCCTGTGTGTGTCACTGCCAGACCGCGCGAAGAGCC 901  
QY 305 ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln 324  
Db 902 ACCTTTTGGAGGTGCGCTCTGCGACGCGCGCTCCCACTCCCACTCCGTTGGGCGCGCG 961  
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Db 962 CACACCGGGGGCGCGCGCTCCACATCGGGCGCACCATGCTCCCTGGGACACGCTTGTCCC 1021  
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QY 365 ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu 384  
Db 1082 CCCTCTCTCTACTCAGCTCTCTGAGGCCAGCGCTGACTGGCGCTCGGAGGCTCGTGAG 1141



QY	385	ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgLeuProArgLeu	404
DB	1142	ACATCTTCTGGGTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTCGCCGCCGTG	1201
QY	405	ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuGlyAsnHisAlaGln	424
DB	1202	CCCCAGCGTACTGGCAATGCGGCCCTGTCTTCTGGAGCTGCTTGGGAACACCGCGCAG	1261
QY	425	CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla	444
DB	1262	TCCCCCTACGGGGTGCTCTCAAGACGCCTCCCGCTCGAGCTCGCGTCAACCCAGCA	1321
QY	445	AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp	464
DB	1322	GCCGGTGTCTGTGCCGGAGAGCCCGCAGGCTCTGTGGCGGCCCGCCGAGGAGGAC	1381
QY	465	ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr	484
DB	1382	ACAGACCCCGCTCGCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCTGGCAGGTGTAC	1441
QY	485	GlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySerArgHis	504
DB	1442	GGCTTCGTGCGGGCTGCTCGCGCGGCTGGTGCCGCCAGGCTCTTGGGGCTCCAGGCAC	1501
QY	505	AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys	524
DB	1502	ACGAAACGGCTTCTTCAGGAACACCAAGAAGTCACTCCCTGGGGAAGCATGCCAAG	1561
QY	525	LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg	544
DB	1562	CTCTCGCTCAGAGCTGACGTGGAAGATGAGCGTGGCGGACTGCGCTTGGCTGGCAGG	1621
QY	545	SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluIleLeuAla	564
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QY	565	LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPheTyr	584
DB	1682	AGTTCTCTGCATGGCTGATGATGTGTACGTGCGAGCTGCTCAGGTCCTTCTTTAT	1741
QY	585	ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer	604
DB	1742	GTCACGGAGACACCGTTTCAAAAGAACAGCGCTTTTCTACCGAAGAGTCTCTGGAGC	1801
QY	605	LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgLeuSer	624
DB	1802	AAGTTGCAAGCATTTGGAATCAGACAGCACTTTGAAGAGGGTGCAGCTGCGGAGCTGCG	1861
QY	625	GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg	644
DB	1862	GAAGCAGAGGTTCAGGACGATCGGAAGCCAGCGCCGCTGCTCAGCTCCAGACTCCGC	1921
QY	645	PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla	664
DB	1922	TTTCATCCCAACCGCTGACGGGTGCGCGCGATGTGTGAACATGCATCGCTGGGAGCC	1981
QY	665	ArgThrPheArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe	684
DB	1982	AGAAGCTTCCGCAGAGAAAAGAGGCGGAGCGTCTCACCTCGAGGGTGAAGCACTGTTC	2041
QY	685	SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly	704
DB	2042	AGCGTGCTCACTACAGCGCGCGCGCCCGCCCTCTCTGGCGCTCTCTGTCTGGGC	2101
QY	705	LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro	724
DB	2102	CTGGAGATATCCACAGGGCTTGGCGACCTTCGTGCTCGGTGGCGGCCCGGAGCCCG	2161
QY	725	ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln	744
DB	2162	CGCCCTGAGCTGTACTTTGTCAAGTTGGATGTGACGGGGCGGTACGACACCATCCCCAG	2221
QY	745	AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg	764
DB	2222	GACAGCTCAGCGAGGTATCGCCAGTATCAAAACCCAGAACACGTACTGCGTGCCT	2281
QY	765	ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis	784
DB	2282	CGSTATGCGTGTCCAGAAGCGCCCATGGCAGCTCCGCAAGGCTTCAAGAGCCAC	2341
QY	785	ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu	804
DB	2342	GTCTCTACCTTGACAGACCTCCAGCGGTATCGCAGTGTCTGTGCTCACCTGCAGGAG	2401
QY	805	ThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGluAlaSer	824
DB	2402	ACAGCCCTCAGGGATCCGTCGTCATCGCAGAGCTCTCTCCCTGAATGAGGCAGC	2461
QY	825	SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly	844
DB	2462	AGTGGCTCTTCGACGTCTCTTCATCGCTTCATGTGTCACACGCGTGGCATCAGGGC	2521
QY	845	LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys	864
DB	2522	NAAGTCTACGTCCAGTCCAGGGGATCCCGCAGGCTCCATCTCTCCACGCTGCTGTC	2581
QY	865	SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgaspGlyLeu	884
DB	2582	AGCTGTGTCAGCGACATGGAGAACAGCTGTTCGCGGGATTTCGGCGGACGGGCTG	2641
QY	885	LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr	904
DB	2642	CTCCTGCGTTTGGTGGATGATTTCTTGTGTTGGTGACACCTCACCTCACCGCGAAACC	2701
QY	905	PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys	924
DB	2702	TTCTCAGAGACCTTGTCGAGGTGCTCTGAGTATGCTGCTGCTGCTGCTGCTGCTG	2761
QY	925	ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet	944
DB	2762	ACAGTGTGAACCTTCCCTGTAGAAGACGAGGGCCCTGGGTGGCAGCGCTTTTGTTCAGATG	2821
QY	945	ProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeuGluVal	964
DB	2822	CCGGCCACCGCTATTCCCTGGTGGCGGCTGCTGCTGATACCCGCGACCTGGAGGTG	2881
QY	965	GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg	984
DB	2882	CAGAGCGACTACTCCAGCTATGCCGACCTCCATCAGAGCCAGTCTCACCTTCAACCGC	2941
QY	985	GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys	1004
DB	2942	GGCTTCAAGGCTGGGAGAACATGCGTCGCAAACTCTTTGGGTCTTGGGCTGTAAGTGT	3001
QY	1005	HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr	1024
DB	3002	CACAGCTGTCTTGGATTGCGAGGTGAACAGCTCCACAGGTGTGACCAACATCTAC	3061
QY	1025	LysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis	1044
DB	3062	AAAGTCTCTCTGTCAGGCGTACAGGTTTTCAGCATGTGTGTCGAGCTCCCATTTTCAT	3121
QY	1045	GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu	1064
DB	3122	CAGCAAGTTTGAAGAACCCCATTTTCTCGCGTCTCTCTGACAGCGCTCCCTC	3181
QY	1065	CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla	1084
DB	3182	TGCTACTCATCTTGAACCAAGAACGAGGATGTGCTGGGGCCGAGGGCGCGCC	3241
QY	1085	GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeu	1104
DB	3242	GGCCCTCTGCCCTCCGAGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3301
QY	1105	ThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGln	1124

Db 3302 ACTCGACACCGGTGTCACCTACGTGTCACCTCTCTGGGGTCACTCAGACAGCCCGACGACG 3361  
Qy 1125 LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsnProAla 1144  
Db 3362 CTGATCGGAAGTCCCGGGACGACGCTGACTGCTGCTGGAGCGCGACCAACCGGCA 3421  
Qy 1145 LeuProSerAspPheLysThrIleLeuAsp 1154  
Db 3422 CTGCCCCACAGCTTCAAGACCATCTGGAC 3451

## RESULT 7

US-09-675-321-1  
; Sequence 1, Application US/09675321  
; Patent No. 6440735  
; GENERAL INFORMATION:  
; APPLICANT: Gaeta, Federico C.A.  
; APPLICANT: Geron Corporation  
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune  
; TITLE OF INVENTION: Response to a Telomerase Antigen  
; FILE REFERENCE: 015389-003500PC  
; CURRENT APPLICATION NUMBER: US/09/675,321  
; CURRENT FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/112,006  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898  
; PRIOR FILING DATE: 1999-03-30  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4015  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (56)..(3454)  
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)  
US-09-675-321-1

Alignment Scores:  
Pred. No.: 0 Length: 4015  
Score: 6057.00 Matches: 1150  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.64% Indels: 0  
DB: 4 Gaps: 0

US-08-951-733-20 (1-1154) x US-09-675-321-1 (1-4015)

Qy 5 GlnArgCysValLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro 24  
Db 2 CAGCGCTGCGTCTGCTGCGACGTGGGAAGCCCTGGCCCGGCGCACCCCGCGATGCGG 61  
Qy 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44  
Db 62 CGGCTCCCGCTGCGGAGCGGTGCTGCTGCGGAGCCACTACCGGAGGTGCTG 121  
Qy 45 ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64  
Db 122 CCGGTGGCCACGTTCGTGCGGCGCTGGGGCCCGCAGGGCTGGGGTGTGTCAGCGCGG 181  
Qy 65 AspProAlaAlaPheArgAlaLeuAlaGlnCysLeuValCysValProTrpAspAla 84  
Db 182 GACCGGCGCTTCGCGCGCTGGTGGCCAGTGGCTGTGCTGCGTGGCCCTGGGACGCA 241  
Qy 85 ArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104  
Db 242 CGCGCGCCCGCGCGCCCTCTCCCGCAGGTGTCTGCTGAGGAGCTGGTGGCC 301  
Qy 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124  
Db 302 CGAGTGTGAGAGGTGTGCGAGCGCGGCGGAACCTGTGCTGGCTTCGCTTCGCG 361

Qy 125 LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr 144  
Db 362 CTGCTGGAGCGGGCGCGGGGCGCCCGCAGGCGCTTCAACACGAGCGTGCAGCTAC 421  
Qy 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuLeuArg 164  
Db 422 CTGCCCCAACACGGTGACCGACGCTGCGGGGAGCGGGCGGTGGGGTGTGCTGCTGCGC 481  
Qy 165 ArgValGlyAspAspValLeuHisLeuLeuAlaArgCysAlaLeuPheValLeuVal 184  
Db 482 CGCGTGGGCGAGCGTGTGCTTCACTGTGCGACGCTGCGCGCTCTTGTGCTGGTG 541  
Qy 185 AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr 204  
Db 542 GCTCCAGCTGCGCTACCGAGTGTGCGGGCGCGCTGTACACAGCTCGGCGCTGCCACT 601  
Qy 205 GlnAlaArgProProHisAlaSerGlyProArgArgLeuGlyCysGluArgAla 224  
Db 602 CAGGCGCGCGCGCGCGCGCGCTAGTGGACCGCGAGGCGTCTGGGATGCGAAGCGGC 661  
Qy 225 TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg 244  
Db 662 TGGAAACATAGCTCAGGAGCGCGGGTCCCGCTGGGCGCTCCAGCGCCCGGGTGGAGG 721  
Qy 245 ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla 264  
Db 722 AGGCGGGGCGAGTGCAGCGCAAGTCTGCGTTGCCAAGAGCGCCAGGCGTGGCGCT 781  
Qy 265 AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr 284  
Db 782 GCCCTTGAGCGGAGCGAGCGCGGTGGGCGAGGGTCTCTGGCGCCACCGCGGCGAGGAC 841  
Qy 285 ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla 304  
Db 842 CGTGGACCGAGTGACCGTGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 901  
Qy 305 ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln 324  
Db 902 ACCTCTTTGGAGGGTGCCTCTCTGCGACGCGCCACTCCACCCACTCTGCGGCGCGCAG 961  
Qy 325 HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro 344  
Db 962 CACCACGGGGCG 1021  
Qy 345 ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg 364  
Db 1022 CCGGTGTAGCGCGAGACCAAGCACTCTCTCTACTCTCTCAGCGGACAGGAGCGAGTGGG 1081  
Qy 365 ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu 384  
Db 1082 CCGCT 1141  
Qy 385 ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu 404  
Db 1142 ACCATCTTCTGGGTTCAGGCGCTTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1201  
Qy 405 ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln 424  
Db 1202 CCGCAGCGCTACTGCGCAATGCGCGCGCTGTCTTCTGGAGCTGTCTTGGAGTGGAGTGGAG 1261  
Qy 425 CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla 444  
Db 1262 TGGCGCTTACGGGTGTCTCTCAGACGCTGCGCGCTGCGAGTGGCGTGGCGTGGCGTGGCG 1321  
Qy 445 AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluGluAsp 464  
Db 1322 CGCGGTGTCTGTGCGCGGAGAGCGCGCGGTCTGTGGCGCGCGCGCGCGCGCGCGCGCG 1381  
Qy 465 ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr 484  
Db 1382 ACAGACCGCGCTGCGCTGGTGCAGTGTCTCGCGCAGCAGCAGCGCGCGCGCGCGCGCG 1441  
Qy 485 GlyPheValArgAlaCysLeuArgLeuValProProGlyLeuTrpGlySerArgHis 504

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Db 1442 GGCCTTCGTGGGGCTGCTGCGCGGCTGGTGGCCCCCAGGCTCTGGGGCTCAGGCAC 1501  
Qy 505 AsnGluArgArgPheLeuArgAsnThrLysLysPheLeuSerLeuGlyLysHisAlaLys 524  
Db 1502 AACGAAGCGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAG 1561  
Qy 525 LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg 544  
Db 1562 CTCTCGCTGCAGGAGCTGACGTGGAGATGAGCGTGGGACTCGCGCTGGCTGGCGAGG 1621  
Qy 545 SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLeuAla 564  
Db 1622 AGCCAGGGGTGGCTGTGTTCCGGCCGACAGACACCTCTCGCTGAGGAGATCCTGGCC 1681  
Qy 565 LysPheLeuHisTrpLeuMetSerValTrpValValGluLeuLeuArgSerPhePheTyr 584  
Db 1682 AAGTTCCTGCACCTGGCTGATGAGTGTACGTCTCGAGCTGCCTCAGGTCTCTCTTTAT 1741  
Qy 585 ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer 604  
Db 1742 GTACAGGAGACCATCTTCAAAAGAACAGGCTCTTTTCTACCGAAGAGTGTCTGGAGC 1801  
Qy 605 LysLeuGlnSerIleGlyLysArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer 624  
Db 1802 AAGTTGCAAGCATTTGAATCAGACACACACTTGAAGAGGTGCAGCTCGGGAGCTGTGG 1861  
Qy 625 GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg 644  
Db 1862 GAACAGAGGTTCAGCAGCATCGGGAAGCCAGGCGCCCTGCTGAGCTCCAGACTCCGC 1921  
Qy 645 PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla 664  
Db 1922 TTATATCCCAAGCTGACGGCTCGGCCGATGTGAACATGGAGTACGTCTGGGAGCC 1981  
Qy 665 ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe 684  
Db 1982 AGAAGCTTCGCAGAGAAAGAGGGCGGAGCGTCTACCTCGAGSGTGAAGGCACCTGTT 2041  
Qy 685 SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly 704  
Db 2042 AGCTGTCTCAACTACGAGCGGGCGCGCGCCCGCGCTCTGGCGGCTCTGTGCTGGGC 2101  
Qy 705 LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro 724  
Db 2102 CTGGACCATATCCACAGGGCTGCGCACCTTCGTGTGCGTGGCGGCCACGAGACCG 2161  
Qy 725 ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln 744  
Db 2162 CCGCTGAGCTGTACTTTGCAAGGTGGATGTGACGGCGCGTACGACACCATCCCCAG 2221  
Qy 745 AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg 764  
Db 2222 GACAGGCTCAGGAGGTTCATCGCCAGCATCATCAACCCCAAGACACGTACTGCGTGGCT 2281  
Qy 765 ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis 784  
Db 2282 CGGTATCCGTGGTCCAGAGGCCGCCCATCGGGCACGTCCCAAGGCTTCAGAGCCAC 2341  
Qy 785 ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu 804  
Db 2342 GTCTCTACCTTGACAGACCTCCAGCCGTACATGGACAGATTCGTGGTCTACCTGCAGGAG 2401  
Qy 805 ThrSerProLeuArgAspAlaValIleGluGlnSerSerLeuAsnGluAlaSer 824  
Db 2402 ACCAGCCGCTGAGGATGCGGTGTCATCGACAGAGCTCTCCCTGAATGAGGCCAGC 2461  
Qy 825 SerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIleArgGly 844  
Db 2462 AGTGGCTCTTCGACGCTCTTCCTACGCTTATGTCGCCACACGCGCGTGCAGATCAGGGC 2521  
Qy 845 LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys 864  
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Db 2572 AAGTCTACGCTCAGTGCCAGGGATCCCGAGGGCTCCATCTCTCCACGCTGCTCTGC 2581  
Qy 865 SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu 884  
Db 2582 AGCTGTGCTACGGCGACATGGAGAACAGCTGTTGGGGGATTCGGCGGAGCGGGCTG 2641  
Qy 885 LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr 904  
Db 2642 CTCTCGCTTGGTGGATGATTTCTGTTGGTGACACCTCACCTCACCACCGCGAAACC 2701  
Qy 905 PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys 924  
Db 2702 TTCCTCAGGACCTTGGTCCGAGGTGCTCCCTGAGTATGCTGCGTGTGAACCTTCGCGAAG 2761  
Qy 925 ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet 944  
Db 2762 ACAGTGGTGAACCTTCCCTGTAGAACACAGGCGCTGGGTGGCAGCGCTTTGTTTTCAGATG 2821  
Qy 945 ProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeuGluVal 964  
Db 2822 CCGGCCACGGCCCTATTCCTCGTGGCGCTGCTGCTGGATACCCCGACCTGGAGGTG 2881  
Qy 965 GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg 984  
Db 2882 CAGAGCGACTACTCCAGCTATGCCGAGACCTCCATCAGAGCGAGTCTCACCTTCAACGCG 2941  
Qy 985 GlyPheLysAlaGlyArgAsnMetArgLysLeuPheGlyValLeuArgLeuLysCys 1004  
Db 2942 GGCCTTCAAGGCTGGGAGAACATGCTGCGCAAACTCTTTTGGGGTCTTGGCGTGAAGTGT 3001  
Qy 1005 HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr 1024  
Db 3002 CACAGCTGTGTTCTGGATTTGCAGGTGAACAGCTCCAGAGCGGTGTGCACCAACATCTAC 3061  
Qy 1025 LysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis 1044  
Db 3062 AAGATCTCTCTGCTGAGCGGTACAGGTTTTCACGATGTGTGCTGACGCTCCCATTTTCA 3121  
Qy 1045 GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu 1064  
Db 3122 CAGCAAGTTTGGAGAACCACACATTTTTCCTGCGCGTCATCTCTGACACGGCTCCCTC 3181  
Qy 1065 CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValAlaLysGlyAlaAla 1084  
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Qy 1085 GlyProLeuProSerGluAlaValIleTrpLeuCysHisGlnAlaPheLeuLeuLysLeu 1104  
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Qy 1125 LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsnProAla 1144  
Db 3362 CTGAGTGGAAAGCTCCCGGGGACGAGCTGACTGCCCTGGAGGCCGCGACCAACCGGCA 3421  
Qy 1145 LeuProSerAspPheLysThrIleLeuAsp 1154  
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Db 3422 CTGCGCTCAGACTTCAAGACCATCCTGGAC 3451

## RESULT 8

US-09-052-919-1

; Sequence 1, Application US/09052919

; Patent No. 6444650

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; APPLICANT: Lingner, Joachim

; APPLICANT: Nakamura, Toru

; APPLICANT: Chapman, Karen B.

; APPLICANT: Morin, Gregg B.

; APPLICANT: Harley, Calvin B.

APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Antisense Compositions for Detecting and  
; TITLE OF INVENTION: Inhibiting Telomerase Reverse Transcriptase  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/052,919  
FILING DATE: 31-MAR-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/974,549  
FILING DATE: 19-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/974,584  
FILING DATE: 19-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Parent, Annette S.  
REGISTRATION NUMBER: 42,058  
REFERENCE/DOCKET NUMBER: 015389-003600US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4015 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 56...3454

OTHER INFORMATION: /product= "human telomerase reverse  
; OTHER INFORMATION: transcriptase (hTERT)"  
US-09-052-919-1  
Alignment Scores:  
Pred. No.: 0 Length: 4015  
Score: 6057.00 Matches: 1150  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.64% Indels: 0  
DB: 4 Gaps: 0  
US-08-951-733-20 (1-1154) x US-09-052-919-1 (1-4015)  
QY 5 GlnArgCysValLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro 24  
|||||  
DB 2 CAGCGCTGGTCTGCTGGCGACGTGGGAAGCCCTGGCCCCCGCCACCCCGCATGGCG 61  
QY 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44  
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DB 62 CGCGCTCCCGCTGCCGAGCGTGGCTCCCTGGCTGGCAGCCACTACCGCGAGTGTGTG 121  
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|||||  
DB 122 CGCGTGGCCACGTTCTGGCGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGCGAGCGGG 181  
QY 65 AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla 84  
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DB 182 GACCGCGGGCTTCCGGCGCGCTGGTGGCCAGTCCCTGGTGGCTGGCTGGCGACGCA 241  
QY 85 ArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104  
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DB 242 CGGCGCGCGCGCGCGCGCGCGCTCCCTCCCTCCGCCAGGTGTCTGTGCTCAAGAGCTGTGGCC 301  
QY 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124  
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DB 302 CGAGTGTGCAGAGGCTGTGGAGCGCGCGCGGAGAACGTGCTGGCTTCGGCTTCGGCT 361  
QY 125 LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr 144  
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DB 362 CTGCTGGACGGGGCGCGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 421  
QY 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuArg 164  
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DB 422 CTGCCCAACACGGTGACCGACGCTGCGGGGAGCGGGGCGGTGGGGCTGTGTGTGGCG 481  
QY 165 ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal 184  
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DB 482 CGCGTGGGCGAGCGAGCTGTGGTTCACCTGTGGCAGCGCTGGCGCGCTCTTTGTGTGTG 541  
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QY	325	HisHisAlaGlyProProSerThrSerArgProProArgProTIPAspThrProCysPro	344	QY	685	SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly	704
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Db	1082	CCCTCTCTCTACTCAGCTCTCTGAGGCCACGCCCTGACTGGCGCTCGGAGGCTGTGGAG	1141	Db	2162	CGCGCTGAGCTTACTTTGTCAAGGTGGATGTGACGGGCGGTACGACACCATCCCCCAG	2221
QY	385	ThrIlePheLeuGlySerArgProTIPMetProGlyThrProArgArgLeuProArgLeu	404	QY	745	AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg	764
Db	1142	ACCATCTTCTGGTTCAGGGCCCTGGATGCCAGGCACTCCCGCAGGTGGCCCGCCTG	1201	Db	2222	GACAGGCTCACGGAGGTATCGCCAGCATCATCAAAACCCAGAACACGTACTCGGTGGT	2281
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QY	425	CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla	444	QY	785	ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu	804
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QY	645	PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla	664	QY	1005	HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr	1024
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RESULT 9

US-08-912-951-1  
Sequence 1, Application US/08912951  
Patent No. 6475789  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND  
TITLE OF INVENTION: THERAPEUTIC METHODS  
NUMBER OF SEQUENCES: 335  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,951  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002600US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4015 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
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NAME/KEY: CDS  
LOCATION: 56..3454  
OTHER INFORMATION: /product= "hTERT"  
OTHER INFORMATION: /note= "human telomerase reverse  
transcriptase (hTERT) catalytic protein  
component"  
US-08-912-951-1

Alignment Scores:

Pred. No.: 0 Length: 4015  
Score: 6057.00 Matches: 1150  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.64% Indels: 0  
DB: 4 Gaps: 0

US-08-951-733-20 (1-1154) x US-08-912-951-1 (1-4015)

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Db 62 CGCGCTCCCGCTGCCAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTG 121  
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Db 962 CACCAGCGGGCCCCCATCCACATCGCGGCCACACACGTCCTTGGGACACGCTGTGCC 1021  
QY 345 ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg 364  
Db 1022 CCGGTGTACCGCGAGACCAAGCACTTCTCTACTCTCTCAGGGCACAAGGAGCAGTCTCGG 1081  
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QY 465 ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr 484  
Db 1382 ACAGACCCCGCTCGCGCTGTGTGAGCTGTCTCCGCCAGCACAGCAGCGCCCTTGGCAGGTGTAC 1441  
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Qy 1045 GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu 1064
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Qy 1065 CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla 1084
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Qy 1085 GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeu 1104
Db 3242 GGCCCTCGCCCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCATTTCTGCTCAAGCTG 3301
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Db 3302 ACTCGACACGCTGTACCTACGTGCCACTCTCTGGGGTCACTCAGGACAGCCAGACGACG 3361
Qy 1125 LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsnProAla 1144
Db 3362 CTGAGTCGGAAGTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGAGCCCAACCCGCA 3421
Qy 1145 LeuProSerAspPheLysThrIleLeuAsp 1154
Db 3422 CTGCCCTCAGACTTCAGACCATCCTGGAC 3451
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## RESULT 10

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US-09-733-294A-3
; Sequence 3, Application US/09733294A
; Patent No. 6492171
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wancewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733, 294A
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (56)...(3454)
US-09-733-294A-3
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## Alignment Scores:

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Pred. No.: 0 Length: 4015
Score: 6057.00 Matches: 1150
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.64% Indels: 0
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US-08-951-733-20 (1-1154) x US-09-733-294A-3 (1-4015)

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Db 2 CAGCGCTGCGTCCCTGCTGGCACGCTGGAGAGCCCTGGCCCGGCGCACCCCGCGCATGGCG 61
Qy 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44
Db 62 CGCGCTCCCGCTCCGAGCGCTGCTCCCTGCTGGCAGCCACTACCGGAGGTGCTG 121
Qy 45 ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64
Db 122 CCGCTGGCCAGCTTCGTGGCGCGCTGGGGGCCCGCAGGCTGCGGCTGGCTGGCGCGGG 181
Qy 65 AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla 84
Db 182 GACCGCGCGGCTTTCGCGCGCTGGTGGCCCGTCCCTGCTGGCTGGCTGGCGAGCA 241
Qy 85 ArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104
Db 242 CGGCGCGCGCGCGCGCGCGCTCCCTCCGCGCAGGTGCTCCCTGAAAGAGCTGGTGCGC 301
Qy 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124
Db 302 CGAGTGTGTGAGAGAGCTGTGCGAGCGCGCGCGGAGAGACGTGCTGGCTTCGGCTTCGCG 361
Qy 125 LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr 144
Db 362 CTGCTGAGCGGGGCGCGCGGGGCGCGCGCGGAGGCTTACACACAGCGTGGCGAGTAC 421
Qy 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuArg 164
Db 422 CTGCCCCAACAGCTGACGACGCTGCGGGGAGCGGGGCTGGGGCTGCTGCTGCGC 481
Qy 165 ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal 184
Db 482 CGCGTGGCGGACGACGTGCTGGTTCACTGCTGGCACGCTGCGCGCTCTTTGCTGCTGCTG 541
Qy 185 AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr 204
Db 542 GCTCCAGCTGCGCTTACCAGTGTGCGGGCGCGCGCTGTACACAGCTCGGCGCTGCCACT 601
Qy 205 GlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGluArgAla 224
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Qy 225 TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyValArg 244
Db 662 TGGAAACCATAGCTCAGGAGGCGCGGGTCCCGCTGGCGCTGCGAGCCCGGGTGGCAGG 721
Qy 245 ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla 264
Db 722 AGGCGCGGGGCGAGTGCACGCGAAGTCTGCCGTGGCCCAAGAGCGCCAGCGTGGCGCT 781
Qy 265 AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr 284
Db 782 GCCCTGAGCGGAGCGAGCGCGCTTGGGCGAGGGTCTGGGGGCCCGCGCGGAGGAGC 841
Qy 285 ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla 304
Db 842 CGTGGACCGAGTGACCGTGGTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 901
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Db	962	CACCACGGGGCCCCCATCCACATCGGGGCCACACAGGTCCTCGGACACGCTTGTCCTC	1021	
QY	345	ProValTyrAlaGluThrIlyHisPheLeuTyrSerSerGlyAspIysGluGlnLeuArg	364	
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Db	1082	CCCTCTCTTCTACTCAGCTCTCTGAGGCCCAACCTGACTGGCGCTCGGAGGCTCGTGAG	1141	
QY	385	ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu	404	
Db	1142	ACCATCTTTCTGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCGCCTG	1201	
QY	405	ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln	424	
Db	1202	CCCCAGCGCTACTGCAATATCGGCCCTGTTCTTCTGGAGCTGCTTGGGAACACACGCGCAG	1261	
QY	425	CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla	444	
Db	1262	TGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCGCTCGAGCTCGGCTCACCCAGCA	1321	
QY	445	AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp	464	
Db	1322	GCCGTTGTGTGCGCGGAGAAGCCCCCAGGCTCTGTGGCGGCCCCCGAGGAGGAC	1381	
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Db	1382	ACAGACCCCGCTGCTGTCAGCTGCTCCGCCACACAGCAGACGCCCCCTGGCAGGTGTAC	1441	
QY	485	GlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySerArgHis	504	
Db	1442	GGCTTCGTGGGGCTGCTGCGCGCGGTGTGTGCCCCCAGGCTCTGGGGCTCCAGGCAC	1501	
QY	505	AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys	524	
Db	1502	AACGAACCGCTTCTCAGGAACACCAAGAAGTTCACTCTCCTGGGGAAGCATGCCAAG	1561	
QY	525	LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg	544	
Db	1562	CTCTCGCTGCAGAGCTGACGTGGAAGATGACCGTCCGGGACTGCGCTTGGCTGGCGCAGG	1621	
QY	545	SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIleLeuAla	564	
Db	1622	ACCCAGGGTGGCTGTGTCGGCGCCGACAGCACCGCTCTCGGTGAGAGATCCTGGCC	1681	
QY	565	LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPheTyr	584	
Db	1682	AAGTTCTCTGCACTGGCTGATGATGTGTACGTGCTGAGCTGCTCAGGCTCTTCTTTAT	1741	
QY	585	ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer	604	
Db	1742	GTACGGAGACACCGCTTTCAAAGAACAGGCTCTTTTCTTACCGGAAGAGTGTCTGGAGC	1801	
QY	605	LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer	624	
Db	1802	AAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTCGGGAGGTGCG	1861	
QY	625	GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg	644	
Db	1862	GAAGCAGAGGTTCAGCACCATCGGGAAGCAGGCCCGCCCTGCTGACGTCCAGACTCCGC	1921	
QY	645	PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla	664	
Db	1922	TTATATCCCAAGCCTTGACGGGCTGGCGCGATGTTGTAACATGAGTACGTCTGGGAGCC	1981	
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Db	2041	AGAACCTTCGCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGCTGAAGCAGCTGTTCC	2041	
QY	685	SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly	704	
Db	2042	AGCGTCTCAACTACGAGCGGGCGCGCCCGCCGCTCTCTGGCGCCTCTGTGCTGGGC	2101	
QY	705	LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro	724	
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QY	725	ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln	744	
Db	2162	CGCCCTGAGCTGTACTTGTCAAGGTGGATGTACGGGGCGGTACGACCACTCCGCCAC	2221	
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Db	2222	GACAGCTCACGGAGTCTATCCAGCATCATCAACCCAGAACAGTACTGCGTGGCT	2281	
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QY	785	ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu	804	
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QY	805	ThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGluAlaSer	824	
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QY	825	SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly	844	
Db	2462	AGTGGCTCTTCGACGCTTCTTACGCTTCTGTGTCACACGCGCTGGGCATCAGGGGC	2521	
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QY	905	PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys	924	
Db	2702	TTCTCTCAGACCTGTGTCGAGGTGCTCTGAGTATGGCTGGGTGAGTGTGCGGAAG	2761	
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Db	2822	CGGGCCACGGCTATTCCCTGGTGGCGCTGCTGCTGATACCCGACCCCTGGAGGTG	2881	
QY	965	GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg	984	
Db	2882	CAGAGCGACTACTCAGCTATCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCCG	2941	
QY	985	GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys	1004	
Db	2942	GGCTTCAAGGCTGGGAGGACATGCTGCCAACTCTTTGGGGTCTTGGCGCTGAAGTGT	3001	
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Db	3002	CACAGCTCTTCTTGATTTGACAGTGAACAGCTCCAGACGCTGTCACCAACATCTAC	3061	
QY	1025	LysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis	1044	

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RESULT 11
US-08-974-549A-343
; Sequence 343, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
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; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0026100S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 343:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4037 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56...3454
; OTHER INFORMATION: /note= "refined sequence of hTERT cDNA"
US-08-974-549A-343

Alignment Scores:
Pred. No.: 0 Length: 4037
Score: 6048.00 Matches: 1148
Percent Similarity: 99.91% Conservative: 1
Best Local Similarity: 99.83% Mismatches: 1
Query Match: 99.49% Indels: 0
DB: 3 Gaps: 0

US-08-951-733-20 (1-1154) x US-08-974-549A-343 (1-4037)
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Qy 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44
Db 62 CGCGCTCCCGCTCCCGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 121
Qy 45 ProLeuAlaThrPheValArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64
Db 122 CCGCTGGCCAGCTTCGTGGCGGCTGGGGCCCGCAGGCTGGCGGTGGCGGTGGCGGTGG 181
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Db 182 GACCCGGCGGCTTTCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 241
Qy 85 ArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104
Db 242 CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 301
Qy 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124
Db 302 CGAGTGTCTGACAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 361
Qy 125 LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr 144
Db 362 CTGCTGACGGGGCGCGCGGGGGCGCGCGGGGGCGCGCGGGGGCGCGCGGGGGCGCGGG 421
Qy 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaThrPglyLeuLeuLeuArg 164
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Db	482	CGCGTGGGGACACACTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGCTGGTG	541
QY	185	AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr	204
Db	542	GCTCCACAGTGCCTTACCAGGTGTGGGGCCCGCTGTACCAGCTGCGCGCTGCCACT	601
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Db	782	GCCCTTGAGCGGAGCGGACGCCCTTGGCAGGGTCTCTGGGCCACCCCGGCGAGCG	841
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QY	305	ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln	324
Db	902	ACCTCTTTGGAGGTGCGCTCTCTGGCACGCGCCACTCCACCCATCCGTGGGCGCGCAG	961
QY	325	HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro	344
Db	962	CACCACGCGGCGCCCATCCACATCGCGGCCACCACGCTCCCTGGGACACGCTTGCTCC	1021
QY	345	ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg	364
Db	1022	CGGGTACCGCGAGACCAAGCACTTCCCTCTACTCTCAGGCGACCAAGAGCAGCTGCGG	1081
QY	365	ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu	384
Db	1082	CCCTCCTTCTACTACGCTCTCTGAGCGCCAGCCTGACCTGGCGCTCGGAGGCTCGTGAG	1141
QY	385	ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu	404
Db	1142	ACCATCTTCTGGGTTCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCGCCTG	1201
QY	405	ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln	424
Db	1202	CCCCAGCGTACTGGCAATGGCGGCCCTTCTTCTGGAGCTGCTGGGAACCAACGCGCAG	1261
QY	425	CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla	444
Db	1262	TGCCCCCTACGGGTGCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCA	1321
QY	445	AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp	464
Db	1322	GCGGGTGTGTGTCGGGAGAGGCCCGGAGGCTGTGTGGGCGGCCCGGAGGAGGAC	1381
QY	465	ThrAspProArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr	484
Db	1382	ACAGACCCCGTGGCTGTGGAGCTGCTCCGCGCACACAGCAGCCCTGGCAGGTGTAC	1441
QY	485	GlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySerArgHis	504
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QY	505	AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys	524
Db	1502	AACGAACGCGCTTCTCAGGAACACCAAGAGTTATCTCCCTCGGGGAAGCATGCCAAG	1561
QY	525	LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg	544
Db	1562	CTCTCGTGCAGGAGTGCAGTGAAGATGAGGTGCGGACTGCGCTTGGCTGCGCAGG	1621
QY	545	SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIleLeuAla	564
Db	1622	AGCCCCAGGGTGGCTGTGTTCGGCGCGCAGACCGCTCTGGTGAAGAGATCCTGGCC	1681
QY	565	LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyr	584
Db	1682	AGTTCTCTGCACCTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGCTCTTCTTTAT	1741
QY	585	ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer	604
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QY	605	LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuLeuArgLeuSer	624
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QY	685	SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly	704
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QY	805	ThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGluAlaSer	824
Db	2402	ACCAGCCCGTGGGGATGCGTGTATCATGAGCAGAGCTCTCCCTGAATGAGGCCAGC	2461
QY	825	SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly	844
Db	2462	AGTGGCTCTTTCAGCGTCTTCCAGCGTTATGTCGCCACCGCCGCTGCCCATCAGGGC	2521
QY	845	LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys	864
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## RESULT 12

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US-08-974-549A-638
; Sequence 638, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
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Alignment Scores:  
Pred. No.: 0  
Score: 5961.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 98.06%  
DB: 3

Length: 3396  
Matches: 1132  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
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APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 336  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
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APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 638:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3396 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..3396  
OTHER INFORMATION: /note= "http-encoding sequence employing  
alternative codon distributions for  
OTHER INFORMATION: E. coli (all genes)"  
US-08-974-549A-638



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QY 763 ValArgArgTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 782  
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QY 783 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 802  
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RESULT 13  
US-08-974-549A-639  
; Sequence 639, Application US/08974549A  
; Patent No. 6166178  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin B.  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,549A  
; FILING DATE: 19-NOV-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted





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RESULT 14
US-08-974-549A-640
; Sequence 640, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
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; FILING DATE: 01-OCT-1996
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> PRIOR APPLICATION DATA:
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> FILING DATE: 18-APR-1997
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> FILING DATE: 01-OCT-1997
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: WO PCT/US97/17885
> FILING DATE: 01-OCT-1997
> ATTORNEY/AGENT INFORMATION:
> NAME: Apple, Randolph Ted
> REGISTRATION NUMBER: 36,429
> REFERENCE/DOCKET NUMBER: 015389-002610US
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: (415) 576-0200
> TELEFAX: (415) 576-0300
> INFORMATION FOR SEQ ID NO: 640:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 3396 base pairs
> TYPE: nucleic acid
> STRANDEDNESS: single
> TOPOLOGY: linear
> MOLECULE TYPE: DNA
> FEATURE:
> NAME/KEY: -
> LOCATION: 1..3396
> OTHER INFORMATION: /note= "hTERT-encoding sequence employing
> OTHER INFORMATION: alternative codon distributions for
> OTHER INFORMATION: yeast (all genes)"
> US-08-974-549A-640
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> Alignment Scores:
> Pred. No.: 0 Length: 3396
> Score: 5961.00 Matches: 1132
> Percent Similarity: 100.00% Conservative: 0
> Best Local Similarity: 100.00% Mismatches: 0
> Query Match: 98.06% Indels: 0
> DB: 3 Gaps: 0
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> Qy 23 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 42
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> Db 1 ATGCCAAGAGCTCCAAGATGTAGAGCTGTTAGATCTTTGTGTGAGATCTCATTATAGAGAA 60
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> Qy 43 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTPArgLeuValGln 120
> |||||
> Db 61 GTTTTCCCAATTGGCTACCTTTTGTTAGAAGATGGGTCCACAAAGGTTGGAGATTGGTTCAA 120
> |||||
> Qy 63 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTirp 82
> |||||
> Db 121 AGAGGTGATCCAGCTGCTTTTAGAGCTTTGGTTGCTCAATGTTTGGTTTGTTCATG 180
> |||||
> Qy 83 ArgAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 102
> |||||

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QY 463 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 482
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QY 483 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 502
DB 1381 GTTATATGGTTTGTAGACCTGTGTGAGAAGATTGGTTCACAGGTTTGTGGGGTCT 1440
QY 503 ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 522
DB 1441 AGACATATGAAGAAGATTTTTCAGAAATACATAAAAAATTATTTCTTTGGGTAAACAT 1500
QY 523 AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 542
DB 1501 GCTAAATGTCTTTTGCAGAAGATTGACTTGGAAAAATGCTGTGTAGAGATTGTGCTGGTTG 1560
QY 543 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 562
DB 1561 AGAAGATCTCCAGGTGTGGTTGTGTTCCAGCTGCTGAACATAGATTGAGAGAAAGAAAT 1620
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DB 2281 TCTCATCTTCTACTTTGACTGATTGCAACCATATATAGACAAATTTGTGCTCATTTG 2340
QY 803 GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGlu 822
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DB 3241 AAATTTGACTAGACATAGAGTTACTTATGTTCCATTTGTTGGTCTTCTTTCAGAACTGCTCAA 3300
QY 1123 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1142
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RESULT 15

US-08-974-549A-641

; Sequence 641, Application US/08974549A

; Patent No. 6166178

; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin B.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 08/974,549A  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 536  
PRIORITY DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIORITY DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIORITY DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
PRIORITY DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIORITY DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIORITY DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIORITY DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIORITY DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIORITY DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 641:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3396 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..3396  
OTHER INFORMATION: /note= "hTERT-encoding sequence employing

OTHER INFORMATION: alternative codon distributions for  
OTHER INFORMATION: yeast (high expressing genes)\*  
US-08-974-549A-641

Alignment Scores:  
Pred. No.: 0 Length: 3396  
Score: 5961.00 Matches: 1132  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 98.06% Indels: 0  
DB: 3 Gaps: 0  
US-08-951-733-20 (1-1154) x US-08-974-549A-641 (1-3396)  
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Db 1 ATGCCAAGAGCTCCAAGATGTAGAGCTTTAGATCTTTGTGTAGATCTCACTACAGAGAA 60  
QY 43 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 62  
Db 61 GTTTTGCCTTGGCTACTTTTCGTTAGAAGATTGGTCCACAGAGTTGGAGATTGGTTCAA 120  
QY 63 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 82  
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QY 103 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysValLeuAlaPheGly 122  
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Db 601 AGAGCTTGAACCACTCTGTAGAGAGCTGGTGTTCATTTGGTGTGGCAGTTGCCAGGT 660  
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QY 263 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly 282  
Db 721 GGTGCTGCTCCAGAACCCAGAAAGAACTCCAGTTGGTCAAGGTTCTTGGGCTCACCAGGT 780  
QY 283 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 302  
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QY 303 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 322  
Db 841 GAAGCTACTCTTTTGGNAGGTGTTGTCTGGTACTAGACACTCTACCCCTCTGTTCGTT 900

QY	323	ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro	342	QY	683	LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal	702
Db	901	AGACAACACACCGTGGTCCACCATTCTTCTAGACCACCAAGACCATGGGACACTCCA	960	Db	1981	TTGTTCTCTGTTTTGAACCTACGAAAGAGCTAGAAGACAGGTTGTTGGGTCTCTGTT	2040
QY	343	CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln	362	QY	703	LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln	722
Db	961	TGTCACACAGTTTACGCTGAACCTAACGACTTCTGTACTCTTCTGCTGCAAGGAACAA	1020	Db	2041	TTGGGTTTGGAGCATTCACAGAGCTTGGAGAACTTTCGTTTGGAGAGTTAGAGCTCAA	2100
QY	363	LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	382	QY	723	AspProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle	742
Db	1021	TTGAGACCACTTCTTGTGTCTCTTTGACCATCTTTGACCTGGTGTAGAAAGATTG	1080	Db	2101	GACCCACCAACCAAGATTGCTACTTCGTTAAGGTTGACGTTACTGGTGTCTAGACACTATT	2160
QY	383	ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	402	QY	743	ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys	762
Db	1081	GTTGAAACTATTCTTGGGTTCTAGACCATTGGACGTACTCCAAGAAGATTGCCA	1140	Db	2161	CCACAAGACAGATTGACTGAAGTTATTGCTTCTATTATTAAAGCCACAAACACATTACTGT	2220
QY	403	ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis	422	QY	763	ValArgArgTyrAlaValValGlnLysAlaHisGlyHisValArgLysAlaPheLys	782
Db	1141	AGATTGCCACAAGATACTGCAAAATGAGACCATTTGTCTTGGAAATTGTTGGGTAACCA	1200	Db	2221	GTTAGAAGATACGCTGTTGTTCAAAGGCTGCTCACGGTCACGTTAGAAAGGCTTTCAG	2280
QY	423	AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	442	QY	783	SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu	802
Db	1201	GCTCAATGTCCATACGCTGTTTGTGAGACTCACTGTCCATTGAGAGCTGCTGTACT	1260	Db	2281	TCTCACGTTCTACTTTGACTGACTTGCAACCATACATGACACAATTCGTTGCTCACATTG	2340
QY	443	ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	462	QY	803	GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu	822
Db	1261	CCAGCTGCTGGTGTGTGCTAGAGAAAAGCCACAAGGTTCTGTTGCTGCCAGAAGAA	1320	Db	2341	CAAGAAACTTCTCCATTGAGAGAGCGTGTGTTATTGAACAATCTTCTCTTTGAACGAA	2400
QY	463	GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln	482	QY	823	AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle	842
Db	1321	GAACACTGACCCAGAAGATTGGTTCATTTGTGAGACAACACTCTTCTCCATGGCAA	1380	Db	2401	GCCTTCTCTGTTTTGTCGACGTTTTCTTGAGATTCATGTGTCCACGCTGTAGAAATT	2460
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Db	1381	GTTTACGSTTTCGTTAGAGCTTGTTTCGAAGATTGTTCCACAGGTTTGTGGGGTTCT	1440	Db	2461	AGAGTAAGTCTTACGTTCAATGTCAGGTATTCCACAAGGTTCTATTCTCTACTCTTG	2520
QY	503	ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	522	QY	863	LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp	882
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QY	543	ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluIle	562	QY	903	LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	922
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QY	643	LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal	662	QY	1003	LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	1022
Db	1861	TTGAGATTCAATCCAAAGCCACAGCGTTTGGAGACCAATTGTTAACATGGGACTACGTTGTT	1920	Db	2941	AAGTGTCACTCTTGTGTTGGACTTGCAAGTTAACTCTTGTGGAACCTGTTTGTACTAAC	3000
QY	663	GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	682	QY	1023	IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	1042
Db	1921	GGTGCTAGAACTTTCAGAACGAAAGAGAGCTGAAAGATTGACTTCTAGAGTTAAGGCT	1980	Db	3001	ATTTACAAGATTGTTGTTGCCAAGCTTACAGATTCCACGCTGTTGTTTGGCAATTGCCA	3060
				QY	1043	PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla	1062

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Db      ||||| 3061 TTCCACCAACAGTTTGGAGAACCAACTTCTCTTGAGAGTTATTTCTGACACTGCT 3120
QY      ||||| 1063 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1082
Db      ||||| 3121 TCTTTGTGTTACTCTATTTTGAAGGTAAGAACGCTGCTATGCTCTTTGGGTGCTAAGGCT 3180
QY      ||||| 1083 AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1102
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Db      ||||| 3241 AAGTTGACTAGACACAGAGCTTACTTACGTTCCATGTTGGGTTCTTTGAGAACTGCTCAA 3300
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Search completed: October 7, 2003, 15:58:26  
Job time : 303.221 secs



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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 7, 2003, 08:34:20 : Search time 117.779 Seconds

(without alignments)

3556.432 Million cell updates/sec

Title: US-08-951-733-14

Perfect score: 5018

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	4996	99.6	4015	3	US-08-974-549A-1
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4	4996	99.6	4015	4	US-08-430-323-224
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44	364.5	7.3	5544	3	US-08-851-843A-68
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#### ALIGNMENTS

#### RESULT 1

US-08-851-843A-224  
; Sequence 224, Application US/08851843A  
; Patent No. 6093809  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: No. 6093809el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/851.843A  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419

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Sequence 642, App  
Sequence 721, App  
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Sequence 111, App

; FILING DATE: 18-APR-1997  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/724,643  
 ; FILING DATE: 01-OCT-1996  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Apple, Randolph T.  
 ; REGISTRATION NUMBER: 36,429  
 ; REFERENCE/DOCKET NUMBER: 015389-002930US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 576-0200  
 ; TELEFAX: (415) 576-0300  
 ; INFORMATION FOR SEQ ID NO: 224:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4015 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 56..3454  
 ; OTHER INFORMATION: /product= "hTrt"  
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 DB 842 CGTGACCGAGTACCGTGGTTTCTGTGTGTGTACCTGCCAGACCCCGCAAGAGCC 901  
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; Sequence 1, Application US/08974549A  
; Patent No. 6166178  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin B.  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
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; FILING DATE: 19-NOV-1997  
; CLASSIFICATION: 536  
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; FILING DATE: 01-OCT-1996  
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; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; PRIOR APPLICATION DATA:  
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; FILING DATE: 09-MAY-1997  
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; FILING DATE: 01-OCT-1997  
; PRIOR APPLICATION DATA:  
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; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:

```

: NAME: Apple, Randolph, Ted
:
: REGISTRATION NUMBER: 36,429
: REFERENCE/DOCKET NUMBER: 015389-0026100S
:
: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: (415) 576-0200
:
: TELEFAX: (415) 576-0300
:
: INFORMATION FOR SEQ ID NO: 1:
:
: SEQUENCE CHARACTERISTICS:
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: LENGTH: 4015 base pairs
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: TYPE: nucleic acid
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: STRANDEDNESS: single
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QY	105	ArgValLeuGlnArgLeuCysGluArgGlyAlaLysValLeuAlaPheGlyPheAla	124
Db	302	CGAGTGTGCAAGAGCTGTGCGAGCGGGGCGAAGAACGTGTGTGCTTGGCTTCGGCTTCGGC	361
QY	125	LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrSerValArgSerTyr	144
Db	362	CTGCTGGACAGGGCCCGGGGGCCCCCGAGGCTTCACCAACAGCGTGGCAGCTAC	421
QY	145	LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuLeuArg	164
Db	422	CTGCCCAACAGGTGACCGACGCACCTGGGGGAGCGGGCGTGGGGGTGCTGTGCTGCGC	481
QY	165	ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal	184
Db	482	CGCGTGGCGCAGCAGCTGCTGGTTCACCTGTGGCACGCTGGCGGCTCTTTGTGTGGTG	541
QY	185	AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr	204
Db	542	GCTCCACGCTGGCCCTACAGGTGTGGGGCCCGCGCTGTACCAGCTGGCGCTGCGACT	601
QY	205	GlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGluArgAla	224

Db 1682 AAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTCTTTTAT 1741  
Qy 585 ValThrGluThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer 604  
Db 1742 GTCACGGAGACACAGTTTCAAAGAACAACAGGCTCTTTTCTACCGAAGAGTGTCTGGAGC 1801  
Qy 605 LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer 624  
Db 1802 AAGTTGCNAACATGTGATCAGACACACTTGAGAGGGTGCAGCTGCGGGAGCTGTCG 1861  
Qy 625 GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg 644  
Db 1862 GAACAGAGGTTCAGGCAGACTCGGAGCAGCCGCCCTGCTGCTGCTCCAGACTCCGC 1921  
Qy 645 PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla 664  
Db 1922 TTCATCCCAAGCCTGACGGCTCGCGCGATTTGAACATGAGTACGTGCTGGGAGCC 1981  
Qy 665 ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe 684  
Db 1982 AGACGTTCAGAGAGAGAGAGGCGCGCTCTACCTCGAGGGTGAAGCACTGTC 2041  
Qy 685 SerValLeuAsnTyrGluArgAlaArgProGlyLeuLeuGlyAlaSerValLeuGly 704  
Db 2042 AGCGTGTCAACTACGAGCGGCGCGCGCCGCTCTGCTGGCGCTCTGTGCGGC 2101  
Qy 705 LeuAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro 724  
Db 2102 CTGACCATATCCACAGGGCTGCGCACCTTCGTGCTGCTGGCGGCCCGCAGACCCG 2161  
Qy 725 ProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln 744  
Db 2162 CCGCTGAGCTGTACTTGTCAAGTGGATGTGAGGGCGGTACGACACCATCCCCAG 2221  
Qy 745 AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg 764  
Db 2222 GACAGGCTCAGGAGGTATCGCCAGCATCATCAACCCAGACACGCTACTGCGTGGT 2281  
Qy 765 ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis 784  
Db 2282 CGGTATGCCGTGGTCCAGAGGCGCCCATGGGACGCTCCCAAGGCTTCAAGAGCCAC 2341  
Qy 785 ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu 804  
Db 2342 GTCTCTACCTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCCTCAGAG 2401  
Qy 805 ThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGluAlaSer 824  
Db 2402 ACCAGCCGCTGAGGGATGCGCTCATCGACGACAGCTCCTCCCTGAATGAGGCCAGC 2461  
Qy 825 SerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIleArgGly 844  
Db 2462 AGTGGCTCTTCGACGCTTCTCTACGCTTTCATGTGCCACACGCGCTGCGCATCAGGGC 2521  
Qy 845 LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys 864  
Db 2522 AAGTCTTACGTCCAGTCCAGGGATCCCGAGGGCTCCATCTCTCCACGCTGCTGTC 2581  
Qy 865 SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu 884  
Db 2582 AGCTGTGTCTACGGCGACATCGAGACAAAGCTGTTCGGGGATTCGGCGGAGCGGCTG 2641  
Qy 885 LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr 904  
Db 2642 CTCCTGCGCTTGGTGGATGATTTCTTGTGTGACACCTCACCTCACCCAGCGCAAAACC 2701  
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Qy 925 ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet 944  
Db 2762 ACAGTGGTGAACCTTCCCTGTAGAGAGACGAGGCCCTGGGTGCACGGCTTTGTTCAGATG 2821

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RESULT 3  
US-08-854-050-224  
; Sequence 224, Application US/08854050  
; Patent No. 6261836  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morlin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: No. 6261836el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/854,050  
; FILING DATE: 09-MAY-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-0029300S  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 224:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4015 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 56...3454 /product= "htrr"  
; OTHER INFORMATION: /note= "human telomerase reverse  
; OTHER INFORMATION: transcriptase (htrr) catalytic protein  
; OTHER INFORMATION: component"  
US-08-854-050-224

**Alignment Scores:**

Pred. No.:	6.31e-264	Length:	4015
Score:	4996.00	Matches:	945
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.56%	Indels:	0
DB:	3	Gaps:	0

US-08-951-733-14 (1-949) x US-08-854-050-224 (1-4015)

QY	5	GlnArgCysValLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro	24
DB	2	CAGCGCTCGTCTCTGCTGCGACGTGGGAAGCCCTGGCCCGGCCACCCCGCATGGCG	61
QY	25	ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu	44
DB	62	CGCGCTCCCGCTCGGAGCGGTGCGCTCCCTGCTGCGCAGGCACCTACCCGAGGTGCTG	121
QY	45	ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly	64
DB	122	CGCTGGCGACGTTCTGCGGGCGCTGGGGCCCCAGGGCTGGCGGTGGTCAGCGCGG	181
QY	65	AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla	84
DB	182	GACCGGGGGCTTCCGGCGCTGTGTGGCCAGTGCCTGGTGTGGTGGCCCTGGACGCA	241
QY	85	ArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla	104
DB	242	CGCGCGCCCGCGCGCCCTCCCTCCGCCCAGGTGCTGCTGAGGAGTGTGTGGCC	301
QY	105	ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla	124
DB	302	CGAGTGTGCAAGAGCTGTGGCAGCGCGCGCGAAGAACGTGCTGGCCTTCGGCTTGGC	361
QY	125	LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr	144
DB	362	CTGTGGACGGGGCCCGGGGGCCCCCGAGGCCCTTCACCCAGCGTGGCGACGTAC	421
QY	145	LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuLeuArg	164
DB	422	CTGCCACACAGGTGACCGACGACCTGCGGGGAGCGGGGCTGGGGCTGCTGCTGGC	481
QY	165	ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal	184
DB	482	CGGTGGCGAGACAGTCTGCTGCTTCACCTGTGCGACGCTGGCGCTCTTGTGTGGTG	541
QY	185	AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr	204
DB	542	GCTCCAGCTCGCTACAGGTGTGCGGGCGCGCGTGTACCAAGCTCGGGCTGCCACT	601
QY	205	GlnAlaArgProProProHisAlaSerGlyProArgArgLeuGlyCysGluArgAla	224
DB	602	CAGCCCGGGCCCCCGCACACGCTAGTGGACCCGGAAGCGCTCTGGGATGCGAACGGCC	661
QY	225	TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg	244
DB	662	TGGAAACATAGCGTCAGGAGCCCGGGTCCCTCTGGGCTTGGCAGCCCGGGTGGAGG	721
QY	245	ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla	264
DB	722	AGCGCGGGGGCAGTGCAGCCGAAGTCTGCGGTGCCAGGCCCGGGTGGCGAGG	781
QY	265	AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr	284
DB	782	GCCCTGAGCGGAGCGAGCCCGGTGGCGAGGGGTCTGGGGCCACCCGGGAGGACG	841
QY	285	ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla	304
DB	842	CGTGGACCGAGTGACCGTGGTTCGTGTGGTGTACCTGCCAGCCCGCGGAGAGCC	901
QY	305	ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln	324

Db	902	ACCTCTTTGGAGGGTGGCTCTCTTGGCAGCGGCCACTCCCACCCATCGTGGCGCGCCAG	961
QY	325	HisHisAlaGlyProProSerThrSerArgProArgProArgProTrpAspThrProCysPro	344
Db	962	CACCACGGGGCCCCCATCCACATCGGGGCCACACACGTCCCTGGGACACGCTTGTCCC	1021
QY	345	ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg	364
Db	1022	CGGGTGTACGGCAGACCAAGCACCTCTCTACTCTCAGGGCACAAGGACAGCTGGG	1081
QY	365	ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu	384
Db	1082	CCCTCTCTCTACTCAGCTCTCTGAGGCCACGCTGACTGGCGCTCGGAGGCTGTGGAG	1141
QY	385	ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu	404
Db	1142	ACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCGCGCTG	1201
QY	405	ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln	422
Db	1202	CCCCACGCGTACTGCCAAATGGCGCCCTGTTCTTGGAGCTGCTTGGGAACCAACGCGCAG	1261
QY	425	CysProTyrGlyValLeuLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla	444
Db	1262	TGCCCCCTACGGGGTCTCTCTCAAGACGCACTGCCGCTGCCAGGTGGGTCACCCCAGCA	1321
QY	445	AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluGluAsp	464
Db	1322	GCGGTGTCTGTGCCGGGAGAACCCCGGGCTCTGTGGCGGCCGCCCGAGGAGGAGGAC	1381
QY	465	ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr	484
Db	1382	ACAGACCCCGCTCGGCTGTGTGACGTGCTCCGCCAGCACACGACGCCCTGGCAGGTGTAC	1441
QY	495	GlyPheValArgAlaCysLeuArgLeuValProProGlyLeuLeuTrpGlySerArgHis	504
Db	1442	GGCTTCTGTGGGGCTGTGCTGCGCGGCTGGTGCCCCCAGGCCCTCTGGGGCTCCAGGCAC	1501
QY	505	AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys	524
Db	1502	AACGAAACCCGCTTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGGAAGCATGCCAAG	1561
QY	525	LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg	544
Db	1562	CTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGGGGGACTGCGCTTGGCTGCGCAGG	1621
QY	545	SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIleLeuAla	564
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QY	565	LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyr	584
Db	1682	AGTTCTTGCACTGGCTGATGAGTGTGTACGTCTGTCAGCTGTCAGGTCTTCTTTTAT	1741
QY	595	ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer	604
Db	1742	GTACGGGAGACACGTTTCAAAACACAGGCTCTTTTTTCTACCGGAGAGATGTCTGGAGC	1801
QY	605	LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer	624
Db	1802	AASTTGCAAGACATTGGAATCAGACAGCACTTGAAGAGGTTGACGTGCGGGAGCTGTCTG	1861
QY	625	GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg	644
Db	1862	GAACGAGGTTGAGGCAGCATCGGGAAAGCAGGCCCGCCCTGCTGTGACGTCCACACTCCGC	1921
QY	645	PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla	664
Db	1922	TTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGACATCGTGTGGGAGCC	1981
QY	665	ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe	684
Db	1982	AGAACTTCGCGAGAAAAAGGGCGGCGCTCTCACCTCAGAGGTGAGGCACTGTCTTC	2041



QY 685 SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly 704  
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QY 705 LeuAspIleHisArgAlaTyrArgThrPheValLeuArgValArgAlaGlnAspPro 724  
DB 2102 CTGGAGATATCCACAGGCGCTGGCGCACTTCGTGTGGCGCCCGAGGCCG 2161  
QY 725 ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln 744  
DB 2162 CGCGCTGAGCTGTACTTCTCAAGTGGATGTGACGGCGCTTACGACACCATCCCGCAG 2221  
QY 745 AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg 764  
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DB 2462 AGTGGCTCTTCGAGCTCTTCATCGCTTCATGTGCCACACGCGGTGCATCAGGCGC 2521  
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QY 925 ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet 944  
DB 2762 ACAGTGGTGAACCTTCCTGTAGAAGACGAGGCCCTGGGTGGCAGCGCTTTTGTTCAGATG 2821  
QY 945 ProAlaHisGlyLeu 949  
DB 2822 CCGGCCACCGGCTA 2836

## RESULT 4

US-09-430-323-224

; Sequence 224, Application US/09430323

; Patent No. 6309867

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: No. 6309867e1 Telomerase

; NUMBER OF SEQUENCES: 225

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/430,323

; FILING DATE: 29-Oct-1999

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph T.

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002930US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 224:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4015 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 56..3454

; OTHER INFORMATION: /product= "hTERT"

; /note= "human telomerase reverse

; transcriptase (hTERT) catalytic protein

; component"

; SEQUENCE DESCRIPTION: SEQ ID NO: 224:

; US-09-430-323-224

; Alignment Scores:

; Pred. No.: 6,31e-264 Length: 4015

; Score: 4996.00 Matches: 945

; Percent Similarity: 100.00% Conservative: 0

; Best Local Similarity: 100.00% Mismatches: 0

; Query Match: 99.56% Indels: 0

; DB: 4 Gaps: 0

; US-08-951-733-14 (1-949) x US-09-430-323-224 (1-4015)

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DB 2 CAGCGCTGGCTCTGCTGCGCAGCGCTGGCGGAGCGCTGGCCCGCCCGCCCGCGGATGCCG 61  
QY 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44  
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QY 45 ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64  
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Db 2462 AGTGGCCTTTCCGACGCTCTTCACGCTTCATGTGCCACACGCGCTGGCATCAGGGGC 2521
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Db 2642 CTCCCTGCGTGTGGTGGATCTTCTTGTGTGTGACACCTCACCTCACCCACGCAAAACC 2701
QY 905 PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys 924
Db 2702 TTCCCTCAGACCCCTGGTCCGAGGTGTCCGTGATGCTGCTGGTGAACCTTGGCGAAG 2761
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## RESULT 5

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US-09-572-423B-3
; Sequence 3, Application US/09572423B
; Patent No. 6331399
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William A. Gaarde
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0462
; CURRENT APPLICATION NUMBER: US/09/572,423B
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3454)
US-09-572-423B-3
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Alignment Scores:
Pred. No.: 6,31e-264 Length: 4015
Score: 4996.00 Matches: 945
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.56% Indels: 0
DB: 4 Gaps: 0
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US-08-951-733-14 (1-949) x US-09-572-423B-3 (1-4015)

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QY 5 GlnArgCysValLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro 24
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QY 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44
Db 62 CGCGCTCCCGCTCGGACCGCTGGCTCCCTGCTGCGCAGGCACCTACCGCAGGTGCTG 121
QY 45 ProLeuAlaThrPheValArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64
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Db 122 CCGCTGGCCACAGTTCGTGCGGGCCCTGGGGCCCCAGGGCTGGCGGCTGGTGCGAGCCGGG 181
QY 65 AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla 84
Db 182 GACCCGGCGGCTTCGCGCGCTGGTGGGCCCACTGCTGCTGGTGGCTGCCCTGGGACGCA 241
QY 85 ArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104
Db 242 CCGCGCGCCCCCGCGCCCCCTCTTCCGCCAGGTGCTGCTGCTGAAGAGCTGGTGGCC 301
QY 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124
Db 302 CAGGTGCTCCAGAGCTGTGCCAGCGCGCGGCGGAAGAACGTGCTGCCCTTGGCTTCGGG 361
QY 125 LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr 144
Db 362 CTGCTGGACGGCGCGCGCGCCCCCCCCAGGGCTTCCACCACGAGCTGGCAGCTAC 421
QY 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaThrProGlyLeuLeuArg 164
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QY 165 ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal 194
Db 482 CCGGTGGGCGACGAGCTGTGTTACCTGCTGGCACGCTGCCGCTCTTTGTGCTGGTG 541
QY 185 AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr 204
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QY 205 GlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGluArgAla 224
Db 602 CAGGCCCGGCCCGCCACACGCTAGTGGACCCCGAAGCGCTGCGGATGCGAAGCGGCC 661
QY 225 TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg 244
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QY 285 ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla 304
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QY 305 ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln 324
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QY 325 HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro 344
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QY 345 ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg 364
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QY 365 ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu 384
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QY 385 ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu 404
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QY 465 ThrAspProArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrPglNValTyr 484  
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QY 725 ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln 744  
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QY 765 ArgTyrAlaValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis 784  
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QY 845 LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys 864  
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QY 865 SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu 884  
Db 2582 AGCTGTGCTACGGCGACATCGAAGCAAGCTGTTTGGGGGATTCGGCGGAGCGGCTG 2641  
QY 885 LeuLeuArgLeuValAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr 904  
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QY 905 PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys 924  
Db 2702 TTCCTCAGGACCTTGGTCCGAGGTGTCCTGAGTATGCTGCTGGTGAACCTTGGGAG 2761  
QY 925 ThrValValAsnPheProValGluAspGluAlaLeuGlyThrAlaPheValGlnMet 944  
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; Sequence 1, Application US/09128354  
; Patent No. 6337200  
; GENERAL INFORMATION:  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Geron Corporation  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants  
; FILE REFERENCE: 015389-003310US  
; CURRENT APPLICATION NUMBER: US/09/128,354  
; CURRENT FILING DATE: 1998-08-03  
; EARLIER APPLICATION NUMBER: US 08/851,843  
; EARLIER FILING DATE: 1997-05-06  
; EARLIER APPLICATION NUMBER: US 08/854,050  
; EARLIER FILING DATE: 1997-05-09  
; EARLIER APPLICATION NUMBER: US 08/911,312  
; EARLIER FILING DATE: 1997-08-14  
; EARLIER APPLICATION NUMBER: US 08/912,951  
; EARLIER FILING DATE: 1997-08-14  
; EARLIER APPLICATION NUMBER: US 08/915,503  
; EARLIER FILING DATE: 1997-08-14  
; EARLIER APPLICATION NUMBER: WO PCT/US97/17618  
; EARLIER FILING DATE: 1997-10-01  
; EARLIER APPLICATION NUMBER: WO PCT/US97/17885  
; EARLIER FILING DATE: 1997-10-01  
; EARLIER APPLICATION NUMBER: US 08/974,549  
; EARLIER FILING DATE: 1997-11-19  
; EARLIER APPLICATION NUMBER: US 08/974,584  
; EARLIER FILING DATE: 1997-11-19  
; EARLIER APPLICATION NUMBER: US 09/052,864  
; EARLIER FILING DATE: 1998-03-31  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4015  
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA
US-09-128-354-1

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## Alignment Scores:

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Pred. No.:      6,31e-264      Length:      4015
Score:           4996.00      Matches:       945
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      99.56%      Indels:    0
DB:               4           Gaps:      0

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US-08-951-733-14 (1-949) x US-09-128-354-1 (1-4015)

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QY      25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44
      |||
DB      62 CGCGCTCCCGCTGCCGAGCCGTGGCTCCCTGCTGCCAGCCACTACCGCGAGGTGCTG 121

QY      45 ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64
      |||
DB      122 CGCGTGGCCACCTTCTGCGCGCTGGGGCCCGCCAGGGCTGGCGCTGGTGCAGCGCGGG 181

QY      65 AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla 84
      |||
DB      182 GACCCGGGGCTTCGCGCGCTGGTGGCCAGTGCCTGGTGGTGGCTGGCCCTGGGACGCA 241

QY      85 ArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysLeuValAla 104
      |||
DB      242 CGCGCGCCCGCCCGCGCCCTTCCTCGCCAGGTGCTCGCTGAAGGAGCTGGTGGCC 301

QY      105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124
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DB      302 CGAGTGTCTGACAGGCTGTGGCAGCGCGCGCGGAGACGTGCTGGCCTTCGGCTTCGGCG 361

QY      125 LeuLeuAspGlyAlaArgGlyProProGluAlaPheThrThrSerValArgSerTyr 144
      |||
DB      362 CTGCTGGAGCGGGCCCGGGGGCCCGCCCGAGGCTTCACCCACCGAGCTGGCGAGCTAC 421

QY      145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuArg 164
      |||
DB      422 CTGCCCAACACAGCTGACCGACGCACTGGCGGGGAGCGGGCGCTGGGGCTGCTGTGGCG 481

QY      165 ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal 184
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DB      482 CCGGTGGCGAGCGAGCTGTGCTTCACTGTGGCAGCGCTGGCGCTCTTTGTGTGGTG 541

QY      185 AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr 204
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DB      542 GCTCCAGCTGGCCCTACCAAGTGTGGGGCGCGCGCTGTACCACTCGGCGCTGCCACT 601

QY      205 GlnAlaArgProProHisAlaSerGlyProArgArgLeuGlyCysGluArgAla 224
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DB      602 CAGGCGCGCCCGCCACACGCTAGTGACCCCGAAGGCGTCTGGGATGCCAAGCGGCGC 661

QY      225 TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg 244
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QY      245 ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgGlyAla 264
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DB      722 AGCGCGGGGGCAGTGCACCGCAAGCTGTGCGTTGCCAAGAGCGCCACGAGCGTGGCGCT 781

QY      265 AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr 284
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DB      782 GCGCCGTGAGCGGAGCGGACGCGCCGTTGGGAGGGGCTCTGGGCGCCACCCCGGCGAGGACG 841

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QY      285 ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluGluAla 304
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DB      842 CGTGGACCGAGTGACCGTGTGTCTGTGTGGTGTACCTGCCAGACCCCGCAAGAAGCC 901

QY      305 ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln 324
      |||
DB      902 ACCTCTTTGGAGGTGGCTCTCTGGCAGCGGCCACTCCACCCTCCGTGGGCCGCCAG 961

QY      325 HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro 344
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DB      962 CACCACGCGGGCCCGCCATCCATCGCGGCCACCACTCCCTGGGACACGCGCTGTGCC 1021

QY      345 ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg 364
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DB      1022 CCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCAGGGGACCAAGGAGCAGCTGCCG 1081

QY      365 ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu 384
      |||
DB      1082 CCCTCTTCTACTCAGCTCTCTGAGGCCACGCTGACTGGCGCTCGGAGGCTCTGTGGAG 1141

QY      385 ThrLeuPheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu 404
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DB      1202 CCCCAGCGCTACTGGCAATGCGGCCCTGTCTTGTGAGCTGCTTGGGAACCAACGCGCAG 1261

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QY      465 ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr 484
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DB      1382 ACAGACCCCGCTGCGCTGTGTCAGCTGCTCCGCCAGCACAGCAGCCCTGGCAGGTGTAC 1441

QY      485 GlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySerArgHis 504
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DB      1442 GCCTTCGTGGGGCTGCTGCGCGGCTGGTGGTGGCCCGAGGCTCTGGGGCTCCAGGCAC 1501

QY      505 AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys 524
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DB      1502 AACGAACGCGCTTCTCTCAGGAACCAAGAGTTCTATCTCCTGTGGGAAGCATGCAAG 1561

QY      525 LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg 544
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DB      1562 CTCTCGCTCAGAGGCTGACGTGGAAGATGAGCGTGGGAGCTGGCGCTTGGCTGGCGCAGG 1621

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DB      1622 ACCCCAGGGTGGTGTGTTCGGCGCGCAGAGCACCGCTCTCGCTGAGGAGATCCTGGCC 1681

QY      565 LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyr 584
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DB      1682 AAGTCTCTGCACCTGGCTGATGAGTGTACGTGCTGCTGAGCTGCTCAGGTCTTCTTTTAT 1741

QY      585 ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer 604
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DB      1742 GTCAGGAGACCACTGTTCCANAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGAGAC 1801

QY      605 LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer 624
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QY      625 GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg 644
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DB      1862 GAAGCAGAGGTGAGGACGATCGGAAGCAGGCGCCGCTGCTGACGTCCAGACTCCGC 1921

QY      645 PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla 664

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; Sequence 1, Application US/09675321
; Patent No. 6440735
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; TITLE OF INVENTION: Response to a Telomerase Antigen
; FILE REFERENCE: 015389-003500PC
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; CURRENT APPLICATION NUMBER: US/09/675,321
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
US-09-675-321-1
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Alignment Scores:

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Pred. No.: 6,31e-264 Length: 4015
Score: 4996.00 Matches: 945
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.56% Indels: 0
DB: 4 Gaps: 0

US-08-951-733-14 (1-949) x US-09-675-321-1 (1-4015)
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QY 45 ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64
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QY 85 ArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104
Db 242 CGCGCGCCCGCCCGCGCCCTCTCTCCGCGCAGGTGCTGCTGCTGAAGAGGTGGTGGCC 301
QY 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124
Db 302 CGAGTGTGTGAGAGGTGTGCGAGCGCGCGCGAAGAACGCTGTGCTGGCTTCGGCTTCGCG 361
QY 125 LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr 144
Db 362 CTGCTGACGGGGCGCGCGGGGCGCCCGCGAGGCTTTCACCGAGCTGCGCGTGCAGGTAC 421
QY 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuArg 164
Db 422 CTCGCCCAACACGTTGACCGACGCTGCGGGGAGCGGGGCGGTGGGGGCTGCTGCTCGCG 481
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Db 482 CGCGTGGGGCAGCAGCTGTGTTTCACTCTGTCGACGCTGCGCGCTCTTTGCTGTGTG 541
QY 185 AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr 204
Db 542 GCTCCAGCTGCGCTTACCAAGTGTGCGGGCCCGCGCTGTACCAAGCTGCGCGTGCACCT 601
QY 205 GlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGluArgAla 224
Db 602 CAGCGCGGGCGCGCGCACCGTGTGACCGCGAGGCGTCTGGGATCGGACGCGGCC 661
QY 225 TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg 244
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662 TGGAAACCATACGGTCAGGAGCGCGGGTCCCGCTGGGCTGCCAGCCCGGGTGGCAGG 721 Db  
245 ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla 264 Qy  
722 AGCGCGGGGCGAGTGCAGCCGAAGTCTGCCGTGGCCAAAGAGCGCCAGCGGTGGCGCT 781 Db  
265 AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr 284 Qy  
782 GCCCCTGAGCCGGAGCGAGCCCGCTGGGCGAGGGTCTGGGGCCCAACCGGGCAGGAGC 841 Db  
285 ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluGluAla 304 Qy  
842 CGTGGACCGAGTACCGGTGGTTCTGTGTGGTGTACCTGCCACACCGCCGAAGAGCC 901 Db  
305 ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln 324 Qy  
902 ACCCTCTTGGAGGTGGCGTCTCTGGCACGCGCCACTCCCAACCATCCGTGGCGCCGAG 961 Db  
325 HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro 344 Qy  
962 CACCACGGGGCCCCCATCCATCGCGGCCACACGCTCCCTGGGACAGCCCTGTGCC 1021 Db  
345 ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg 364 Qy  
1022 CCGGTGTACCGCGAGACCAAGCACTTCTTACTCTCCTCAGCGCACAGGACACGCTCGG 1081 Db  
365 ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgLeuValGlu 384 Qy  
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1142 ACCATCTTCTGGGTTCAGGCGCTGGATGCCAGGGACTCCCGCAGAGTGGCCCGCGCTG 1201 Db  
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1202 CCCCAGCGCTACTGGCAATCGCGCCCTGTTCTGGAGCTGCTTGGGAACACCGCGCAG 1261 Db  
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585 ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer 604 Qy  
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1742 GTCACGAGACACCGTTCAAAAGAACAGAGCTCTTTTCTACCGAAGAGTGTCTGGAGC 1801 Db  
605 LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer 624 Qy  
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685 SerValLeuAsnTyrGluArgAlaArgProGlyLeuLeuGlyAlaSerValLeuGly 704 Qy  
2042 AGCGTGTCTAACTACGAGCGCGCGCGCCCGCTCTCTGGGCGCTCTGTCTGGGC 2101 Db  
705 LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro 724 Qy  
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725 ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln 744 Qy  
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2222 GACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGAACACGCTACTGCTGGCT 2281 Db  
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2282 CGGTATGCGGTGGTCCAGAGCGCCCGCATGGGACGCTCCGCAAGGCTTCAAGAGCCAC 2341 Db  
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2702 TTCCTCAGGACCTTCCCTGAGGAGTGTCCCTGAGTATGGCTGGCTGGTGAAGTTCGGA 2761 Db  
925 ThrValValAsnPheProValGluAspGluAlaLeuGlyThrAlaPheValGlnMet 944 Qy  
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945 ProAlaHisGlyLeu 949 Qy  
2822 CCGGCCCCAGGCCCTA 2836 Db



RESULT 8  
US-09-052-919-1  
Sequence 1, Application US/09052919  
Patent No. 6444650  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin B.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Antisense Compositions for Detecting and  
Inhibiting Telomerase Reverse Transcriptase  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/052,919  
FILING DATE: 31-MAR-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/974,549  
FILING DATE: 19-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/974,584  
FILING DATE: 19-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Parent, Annette S.  
REGISTRATION NUMBER: 42,058  
REFERENCE/DOCKET NUMBER: 015389-00360005  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4015 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 56..3454  
OTHER INFORMATION: /product= "human telomerase reverse  
transcriptase (htrt)"  
US-09-052-919-1  
Alignment Scores:  
Pred. No.: 6,31e-264 Length: 4015  
Score: 4996.00 Matches: 945  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.56% Indels: 0  
DB: 4 Gaps: 0  
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QY 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44  
DB 62 CGCGCTCCCGCTGCCGAGCCGCTCCCTGCTGCCGAGCCACTACCGCAGGTGCTG 121  
QY 45 ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64  
DB 122 CGCGTGGCCACGTTCTGCGCGCTGGGGCCCGCAGGGCTGGCGCTGGTGCAGGCGGG 181  
QY 65 AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla 84  
DB 182 GACCGGGGGCTTTCGGCGCTGGTGGCCAGTGCCTGGTGGTGGCTGGCGGACGCA 241  
QY 85 ArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysLutLeuValAla 104  
DB 242 CGGCGCCCGCCCGCCCTCTCCGCCAGGTGCTCTGCTGAAGGAGCTGTGGGCC 301  
QY 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124  
DB 302 CGAGTGTGCAGAGGCTGTGCGAGCGCGCGCGCGGCGGCGGCTGGCTTCGGCTTCGCG 361  
QY 125 LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr 144  
DB 362 CTGCTGGACGGGGCCCGGGGGCCCCCGGAGGGCTTCACCCAGCGGTGGCGAGCTAC 421  
QY 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuArg 164  
DB 422 CTGCCCAACACGGTGACCGACACTGCGGGGGAGCGGGGGCTGGTGGTGGCGC 481  
QY 165 ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal 184  
DB 482 CCGTGGGGCGAGCGTGTGTTTCCCTGCTGGCAGCGTGGCGCTGCTTGTGGTGGG 541  
QY 185 AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr 204  
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QY 205 GlnAlaArgProProHisAlaSerGlyProArgArgLeuGlyCysGluArgAla 224  
DB 602 CAGCGCCCGCCCGCCACACTAGTGGACCCCGAAGGCGCTCTGGGATGCCAGCGGCC 661  
QY 225 TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg 244  
DB 662 TGGAAACCATAGCGTCAGGAGCGCGGGGTGCCCTGGGCGCTGCCAGCCCCGGTGGAGG 721

QY	245	ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla	264
DB	722	AGCCCGGGGGCAGTGCAGCCGAAGTCTGCGGTTCGCCAAGAGGCCAGGCGTGCGCT	781
QY	265	AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr	284
DB	782	GCCCTTGAGCGGAGCGAGCCCGCTTGCGCAGGGGTCTCTGGGCCACCCGGGCGAGGAG	841
QY	285	ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla	304
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QY	305	ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln	324
DB	902	ACCTCTTGGAGGGTGGCTCTCTGGCAGCGCCCACTCCACCACATCCCTGGGGCGCCAG	961
QY	325	HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro	344
DB	962	CACCACGGGGCCCCCATCCACATCGCGGCCACCACCTCCCTGGGACACGCTTGTCCC	1021
QY	345	ProValTrpAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg	364
DB	1022	CCGGTGTACGGCGAGACCAAGCATTCTCTACTCTCAGGGCGACAAGGAGCAGCTGGG	1081
QY	365	ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu	384
DB	1082	CCCTCTCTCTACTCAGCTCTCTGAGGGCCAGCCTGACTGGCGCTCGGAGGCTCGTGAG	1141
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DB	1142	ACCATCTTCTGGGTTCAGGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCGCCCTG	1201
QY	405	ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln	424
DB	1202	CCCCAGCGCTACTGCAATGCGGCCCTGTGTCTCTGGAGCTGCTTGGGAACACACGCGAG	1261
QY	425	CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla	444
DB	1262	TGCCCCCTACGGGGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCA	1321
QY	445	AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp	464
DB	1322	GCCGGTGTCTGTGCCGGGAGAAGCCCGAGGCTCTGTGGCGGCCCGCCAGGAGGAGC	1381
QY	465	ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr	484
DB	1382	ACAGACCCCGTCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCTTGGCAGGTGTAC	1441
QY	485	GlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySerArgHis	504
DB	1442	GGCTTCGTGGGGCCCTGCTGGCGCCGCTGTGTGCCCCAGGCTCTGGGGCTCCAGGCAC	1501
QY	505	AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys	524
DB	1502	AACGAACCGGCTTCTCAGGAACACCAAGAAGTTCTATCTCCCTGGGGAAGCATGCCAAG	1561
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DB	1562	CTCTCGCTGCAGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGGCTTGGCTGGCAGG	1621
QY	545	SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluIleLeuAla	564
DB	1622	AGCCAGGGGTGGGTGTGTCCGGCCCGAGAGCACCGTCTCGGTGAGAGATCTTGCC	1681
QY	565	LysPheLeuHisTrpLeuMetSerValTrpValValGluLeuLeuArgSerPheTyr	584
DB	1682	AAGTTCCTGCACCTGATGAGTGTACGTCTGTCGAGCTGCTCAGGTCTTCTTTTAT	1741
QY	585	ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer	604
DB	1742	GTCACTGGAGACCACTTTCAAAGAACAAGCTCTTTTCTTACCGGAAGAGTGTCTGGAGC	1801

RESULT 9

QY	605	LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer	624
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QY	625	GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg	644
DB	1862	GAAGCAGAGTTCAGCAGCATCGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGC	1921
QY	645	PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla	664
DB	1922	TTCATCCCCAACCCCTGACGGGTGCGCGGATTGTGAACATGACTACCTCTGTGGAGGC	1981
QY	665	ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe	684
DB	1982	AGAACGTTCCGAGAGAAAAGAGGCCGAGCGTCTCACTCGAGGTGAAGCAGCTGTTC	2041
QY	685	SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly	704
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QY	705	LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro	724
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QY	745	AspArgLeuThrGluValIleAlaSerIleLeuLysProGlnAsnThrTyrCysValArg	764
DB	2222	GACAGGCTCACGGAGTTCATCGCAGCATCATCAAAACCCAGACACGTACTGCGTGGCT	2281
QY	765	ArgTyrAlaValValGlnLysAlaHisGlyHisValArgLysAlaPheLysSerHis	784
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QY	785	ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu	804
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QY	805	ThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGluAlaSer	824
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QY	845	LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys	864
DB	2522	AGTCTCTAGTCCAGTCCCGAGGGATCCCGCAGGGCTCCATCTCTCCACGTGCTCTGC	2581
QY	865	SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu	884
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QY	885	LeuLeuArgLeuValValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr	904
DB	2642	CTCCTCGGTTTGGTGGATGATTTCTTGTGTGGTGCACACCTCACCTCACCCACGCAAAAC	2701
QY	905	PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys	924
DB	2702	TTCCTCAGAGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGGCTGGAACCTTGGGAAG	2761
QY	925	ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet	944
DB	2762	ACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATG	2821
QY	945	ProAlaHisGlyLeu	949
DB	2822	CCGGCCCCAGGCCTA	2836



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QY 325 HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro 344
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QY 525 LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg 544
Db 1562 CTCCTCGCTCAGGAGCTGACGTGGAAGATGAGCGTCGGGACTGCGCTTGGTCGCGCAGG 1621
QY 545 SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluLeuLeuAla 564
Db 1622 AGCCAGGGGTGGCTGTGTTCCCGCGCAGAGCACCTCTCGGTGAGGAGATCCTGGCC 1681
QY 565 LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyr 584
Db 1682 AAGTTCCTCGCACTGGCTGATGAGTGTACGTGCTGAGCTGCTCAGGCTCTTCTTTTAT 1741
QY 585 ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer 604
Db 1742 GTCAGGAGACCACTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGC 1801
QY 605 LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer 624
Db 1802 AAGTTCAAAGCAATTGGAATCAGACAGCACTTGAAGAGGTGTCAGCTCGGAGGTGTCG 1861
QY 625 GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg 644
Db 1862 GAAGCAGAGGTTCAGCAGCATCGGAAGCCAGGCGCCCTGCTGACGTCCAGACTCCGC 1921
QY 645 PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla 664
Db 1922 TTATCCCAAGCCTGACGGCTGCGGCCGATTTGGAACATGAGACTAGCTGCTGGAGCC 1981
QY 665 ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe 684
Db 1982 AGAACGTTCCCGCAGAGAAAAGAGGCCGAGGCTCTACCTCGAGGGTGAAGGCAGTGTTC 2041
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QY 685 SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly 704
Db 2042 AGCGTGTCTCAACTAGCAGCGCGCGGCCCGCCCTCTCTGGGCGCCTCTGTGTGGGC 2101
QY 705 LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro 724
Db 2102 CTGGAGCATATCCACAGGGCTTGGCGACCTTCTGTGTGTGTGTGGGCGCCAGGACCG 2161
QY 725 ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln 744
Db 2162 CCGCCTGAGCTGACTTGTCTAAGGTGGATGTGACGGGCGCTAGCACACCATCCCCAG 2221
QY 745 AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg 764
Db 2222 GACAGGCTCACGGAGGTTCATCGCCAGCATCATCAACCCCAAGACGCTACTGCGTGT 2281
QY 765 ArgTyrAlaValIleGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis 784
Db 2282 CGGTATGCGTGTCTCCAGNAGGCCCGCCCATGGCAGCTCCGCAAGCCCTTCAAGAGCCAC 2341
QY 785 ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu 804
Db 2342 GTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTGCTGTGCTCACCTGCGAG 2401
QY 805 ThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGluAlaSer 824
Db 2402 ACCAGCCGCTGAGGAGTCCGCTGTCATCGACGAGAGTCTCTCCCTGAATGAGGCCAGC 2461
QY 825 SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly 844
Db 2462 AGTGGCCTCTTCGACGCTCTTCTACGCTTCATGTGCCACCGCGCTGGCATCAGGGC 2521
QY 845 LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys 864
Db 2522 AAGTCTCAGTCCAGTCCAGGGGATCCCGCAGGCTCCATCTCTCCACGCTGCTCTGC 2581
QY 865 SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu 884
Db 2582 ACCCTGTGCTACGGCGACATGGAGAACAAAGCTGTTTGGGGGATTCGGCGGACGGGCTG 2641
QY 885 LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr 904
Db 2642 CTCCTCGCTTGTGTGATGATTTCTTGTGTGTGACACCTCACCTCACCGCGGAAACC 2701
QY 905 PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys 924
Db 2702 TTCTCTCAGGACCTGCTCGAGGTGCTCCCTGAGTATGCTGTGCTGTAACCTTGGGAAG 2761
QY 925 ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet 944
Db 2762 ACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCAGCGCTTTTTCAGATG 2821
QY 945 ProAlaHisGlyLeu 949
Db 2822 CCGGCCACCGGCTA 2836
RESULT 10
US-09-733-294A-3
; Sequence 3, Application US/09733294A
; Patent No. 6492171
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wancewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 3
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;
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)...(3454)
US-09-733-294A-3
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**Alignment Scores:**

Pred. No.:	6.31e-264	Length:	4015
Score:	4996.00	Matches:	945
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.56%	Indels:	0
DB:	4	Gaps:	0

US-08-951-733-14 (1-949) x US-09-733-294A-3 (1-4015)

QY	5	GlnArgCysValLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro	24
DB	2	CAGCCCTCGCTCTCTCGCACGTGGGAAGCCCTGGCCCGGCACACCCCGGATGCCG	61
QY	25	ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu	44
DB	62	CGCGTCCCGCTGCCGAGCGTGGCTCCCTGCTGCGCAGCCACCTACCCGAGGTGCTG	121
QY	45	ProLeuAlaThrPheValArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly	64
DB	122	CGCGTGGCCAGGTCGTGCGCGCGCTGGGGGCCCCAGGGCTGGCGGTGGTGCGACGCGGG	181
QY	65	AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla	84
DB	182	GACCCGGGGGCTTCCCGCGCGCTGGTGGCCAGTGCCTGTGTGCGTGCCTCGGACGCA	241
QY	85	ArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla	104
DB	242	CGCGCGCCCCCGCGGCCCTCTTCGCCAGGTGCTTGCCTGAAGAGACTGGTGGCC	301
QY	105	ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla	124
DB	302	CGAGTGCCTGCAGAGGCTGTGCGAGCGGGCGGCGAAGAACGTGTGGCTTCGGCTTCGGG	361
QY	125	LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr	144
DB	362	CTGTGTGACGGGGCCCCGGGGGGCCCCCGAGGCCCTCACACACAGCTGGCGACTAC	421
QY	145	LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuLeuArg	164
DB	422	CTGCCAACACGGTGAACGACGCATCTGGGGGAGCGGGCGCTGGGGCTGCTGCTGC	481
QY	165	ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal	184
DB	482	CGCTGGGCGACGACGTGTGGTTCCTGTGCACGCTGCGCGCTCTTTGTGTGGTG	541
QY	185	AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr	204
DB	542	GCTCCCACTGGCCCTACCAAGGTGTGGGGCGCGCTGTACAGCTCGCGCTGCCACT	601
QY	205	GlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGluArgAla	224
DB	602	CAGGCGCGCGCGCGCCACACGCTTGTGTGAGACCCCGAAGGCGTCTGGATGCGAAGCG	661
QY	225	TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg	244
DB	662	TGGAAACCATAGGTCAGGAGGCGGGGGTCCCCCTGGGCGCTGCACGCCCGGGTGGG	721
QY	245	ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgGlyAla	264
DB	722	AGGCGGGGSCAGTGCACGACCGAAGTCTCCGCTGCCCAAGAGGCCAGGCGTGGCGT	781
QY	265	AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr	284
DB	782	CGCCCTGAGCGGAGCGAGCCGCTTGGCAGGGGTCTTGGGCCACCGCGGACGAGCG	841

QY 645 PheileProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla 664  
DB 1922 TTCAATCCCAACCGCTGCGCGCGATGTTGACATGAGTACGTCTGCTGGAGCC 1981  
QY 665 ArgThrPheArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe 684  
DB 1982 AGACGTTCCGAGAGAAAGAGCGCGGCTCTCACTCGAGGGTGAAGCACTGTC 2041  
QY 685 SerValLeuAsnTyrGluArgAlaArgProGlyLeuLeuAlaSerValLeuGly 704  
DB 2042 ACGGTGCTCACTACAGCGCGCGCGCGCGCGCTCTGCGCGCTCTGCTGGGC 2101  
QY 705 LeuAspAspIleHisArgAlaTyrPheValLeuArgValArgAlaGlnAspPro 724  
DB 2102 CTGGAGCATATCCAGAGCGCTGGCGACCTTCGTGCTGCGTGGCGCCAGACCG 2161  
QY 725 ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln 744  
DB 2162 CGGCTGAGCTACTTGTCAAGGTGATGTGACGGCGGTACGACACCATCCCCAG 2221  
QY 745 AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg 764  
DB 2222 GACAGGCTCACGGAGGTATCCCGACATCATCAACCCCAAGACACCTACTGCTGGCT 2281  
QY 765 ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis 784  
DB 2282 CGGTATGCGGTGTCAGAGCGCGCGCATGCGCACGTCCGCAAGCGCTTCAAGAGCCAC 2341  
QY 785 ValSerThrLeuThrAspGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu 804  
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QY 805 ThrSerProLeuArgAspAlaValIleGluGlnSerSerLeuAsnGluAlaSer 824  
DB 2402 ACCAGCGCGCTAGGGATGCGCTCATGCGACAGAGCTCTCCCTGAATGAGGCCAGC 2461  
QY 825 SerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIleArgGly 844  
DB 2462 AGTGGCCCTTCGAGCTCTCTACGCTTCATGTCGCCACCGCGTGGCATCAGGGCC 2521  
QY 845 LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys 864  
DB 2522 AAGTCTACGTCCAGTCCAGGGATCCCGAGGCTCCATCTCTCCACGCTGCTCTGC 2581  
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DB 2582 AGCCTGTGCTACGGCGACATGAGAACAAAGCTGTTTGGCGGGATTTCGGCGGACGGCTG 2641  
QY 885 LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr 904  
DB 2642 CTCCTGCGTGTGGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCACCGAAACC 2701  
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DB 2702 TTCCTCAGGACCTGCTCGAGGTGCTCCCTGAGTATGCTGCTGGTGGTGAACCTGCGAAG 2761  
QY 925 ThrValValAsnPheProValGluAspGluAlaLeuGlyThrAlaPheValGlnMet 944  
DB 2762 ACAGTGGTGAATTCCTCTGTAGAAGACGAGCGCTGGTGGCAGCGCTTTTGTTCAGATG 2821  
QY 945 ProAlaHisGlyLeu 949  
DB 2822 CGGGCCACGGGCTA 2836

## RESULT 11

US-08-974-549A-343  
; Sequence 343, Application US/08974549A  
; Patent No. 6166178

## ; GENERAL INFORMATION:

; APPLICANT: Cecch, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.

Alignment Scores: 1.35e-263 Length: 4037  
Pred. No.:  
US-08-974-549A-343

; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin B.  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,549A  
; FILING DATE: 19-NOV-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 343:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4037 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 56..3454  
; OTHER INFORMATION: /note= "refined sequence of hTERT cDNA"

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Best Local Similarity:	99.89%	Mismatches:	1
Query Match:	99.44%	Indels:	0
DB:	3	Gaps:	0
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DB	2	CAGCGCTGGCTCTGCTGGCAGCTGGAGCCCTGGCCCCGGCCAGCCCGCGATGCCG	61
QY	25	ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu	44
DB	62	CGGCTCCCGCTGGCGAGCGTGGCGCTCCCTGCTGGCAGCCACTACCGGAGGTGCTG	121
QY	45	ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly	64
DB	122	CCGCTGGCCAGCTTCGTGGCGCCCTGGGGCCCCAGGGCTGGCGGTGGTGGCAGCGGG	181
QY	65	AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla	84
DB	182	GACCCGGGCTTTCGCGCGCTGGTGGCCAGTGGCTGGTGGCTGGCGGAGCA	241
QY	85	ArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla	104
DB	242	CGCCCGCCCCCGCCCGCTCTCTTCGCGCAGGTGCTCTGCTGAAAGGAGCTGGTGGCC	301
QY	105	ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla	124
DB	302	CGAGTGTGAGAGGTGTGCGAGCGCGCGCGAAGACGTGCTGGCCTTCGGCTTCGCG	361
QY	125	LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr	144
DB	362	CTGCTGAGCGGGCCCGCGGGGCCCCCGAGGCCCTTCACACAGAGCTGGCCAGCTAC	421
QY	145	LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuArg	164
DB	422	CTGCCCAACACGGTGACCGACACTGCGGGGAGCGGGGCTGCTGCTGCGCG	481
QY	165	ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal	194
DB	482	CGGCTGGGCGACACGTGCTGTACCTGCTGGCAGCTGCGCGCTCTTGTGTGGTG	541
QY	185	AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr	204
DB	542	GCTCCAGCTGCGCTTACCAGGTGTGCGGCGCCGCTGTACACAGCTGCGCGCTGCCACT	601
QY	205	GlnAlaArgProProHisAlaSerGlyProArgArgLeuGlyCysGluArgAla	224
DB	602	CAGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGCGCTGCGGATCGGAACGGCC	661
QY	225	TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg	244
DB	662	TGAACCATAGCTCAGGAGCGCGGGTCCCTGGGCTGCGACCCCGGGTGGGAGG	721
QY	245	ArgArgGlyClySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla	264
DB	722	AGCGCGGGGCGAGTCCAGCCGAACTGTGCCCTGCCCAAGAGCCCGCGCTGGCGCT	781
QY	265	AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr	284
DB	782	GCCTCTGAGCGGAGCGGACGCCGTTGGCAGGGGTCTGGGCCCCACCCGGGCGAGCG	841
QY	285	ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla	304
DB	842	CGTGGACCGAGTGACCGTGGTTCTGTGTGGTGTACCTGCCACAGCCCGCGAAGGCC	901
QY	305	ThrSerLeuGluClyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln	324
DB	902	ACCTCTTTGGAGGTGCGCTCTCTGCGACGCGCCACTCCACCCATCCGTGGGCGCCAG	961
QY	325	HisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrProCysPro	344

Db	962	CACCACGGGCCCCCATCCACATCGCGCCACCAGCTCCCTGGGACACGCTGTGCC	1021
QY	345	ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg	364
DB	1022	CCGTTGTACCGCGAGACCAGACATTCTCTACTCTCAGCGACACAGGACAGCTGCGG	1081
QY	365	ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu	384
DB	1082	CCCTCTCTCTACTCTAGCTCTCTGAGGCCAGCCAGCTGACTGGCGCTCGAGGCTCGTGGAG	1141
QY	385	ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu	404
DB	1142	ACCATCTTTCTGGGTTCAGGCCCTGGATGCCAGGACTCCCGCAGGTGTGCCCGCTG	1201
QY	405	ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisAlaGln	424
DB	1202	CCCCAGCGCTACTGGCAAAATGCGGCCCTGTTCTGGAGCTGCTGGGAACACGCGCAG	1261
QY	425	CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla	444
DB	1262	TGCCCCCTACGGGTGCTCTCAAGACGCACTGCCCGCTGGAGCTGGGTACCCCGACCA	1321
QY	445	AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp	464
DB	1322	GCCGGTGTCTGTCGCGGGAGAACCCAGGGCTCTGTGGCGGCCCGCAGGAGGAGAC	1381
QY	465	ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr	484
DB	1382	ACAGACCCCGCTGCGCTGGTGGCTGCTCCGCCACACAGCAGCCCTGGCAGGTGTAC	1441
QY	485	GlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySerArgHis	504
DB	1442	GGCTTGTGGGGCTTGCCTGCGCGGCTGGTGGCCCCCAGGCCCTCTGGGGCTCCAGGCAC	1501
QY	505	AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys	524
DB	1502	AACGAACCGCGCTTCTCAGAAACACCAAGAGTTTCATCTCCCTGGGGAAGCATGCCAAG	1561
QY	525	LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg	544
DB	1562	CTCTCGCTGCGAGAGTGTAGTGGAAAGTGGCGTGGGAGCTGCGCTTGGCTGGCGAGG	1621
QY	545	SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLeuAla	564
DB	1622	AGCCAGGGGTGGCTGTGTTCCGGCGCAGACACCGCTCTGGTGGAGAGATCCTGGCC	1681
QY	565	LysPheLeuHisTrpLeuMetSerValValValGluLeuLeuArgSerPhePheTyr	584
DB	1682	AACTTCTGCACTGGGTGATGAGTGTAGTGTGCTGCTGAGTGTCTTCTTTTAT	1741
QY	585	ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer	604
DB	1742	GTCAAGAGACACAGCTTCAAAAGAACAGGCTCTTTTCTACCGCGGAGTGTCTGGAGC	1801
QY	605	LysLeuGlnSerIleGlyIleArgGlnHisLysArgValGlnLeuArgGluLeuSer	624
DB	1802	AACTTGCAAGCAATGGAATCAGACAGCACTTGAAGAGGTGGAGCTGCGGGAGCTGTGCG	1861
QY	625	GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg	644
DB	1862	GAAGCAGAGGTGAGCAGCATCGGAAGCCAGGCCCGCTGCTGAGTGTCCAGACTCCCG	1921
QY	645	PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla	664
DB	1922	TTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCTGTGGAGCC	1981
QY	665	ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe	684
DB	1982	AGACGTTCCGACAGAAAGAGGGCGGCTCTCCTCTGAGGGTGAAGGACACTGCTTC	2041
QY	685	SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly	704



Db 2042 AGCGTGCTCAACTACGAGCGGGCGGCCGCCCTCTGGGGCCCTCTGTGCTGGGC 2101  
QY 705 LeuaspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro 724  
Db 2102 CTGGACGATATCCACAGCGCGCTGGCGCACCTTCGTGCTGGCGGCCCGAGACCGC 2161  
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Db 2222 GACAGGCTCAGCGAGGTATCGCCAGCATCATCAAAACCCAGACACGTACTGCGTGGT 2281  
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Db 2582 AGCCTGTCTCAGCGGACATGAGAAACAGCTGTTTGGGGGATTCGCGGGACGCGGTG 2641  
QY 885 LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr 904  
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QY 905 PheLeuArgThrLeuValArgGlyValProGluTyGlyCysValValAsnLeuArgLys 924  
Db 2702 TTCCTCAGACCTTGGTCCGAGGTCTCCCTGAGTATGCTCGGTGGTGAACCTTGGGAG 2761  
QY 925 ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet 944  
Db 2762 ACAGTGTGAACTCCCTGTAGAACGACGAGCGCCCTGGGTGGCAGCGCTTTTGTTCAGATG 2821  
QY 945 ProAlaHisGlyLeu 949  
Db 2822 CGGCCCCACGGCCTA 2836

## RESULT 12

US-08-974-549A-638

; Sequence 638, Application US/08974549A

; Patent No. 6166178

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; APPLICANT: Lingner, Joachim

; APPLICANT: Nakamura, Toru

; APPLICANT: Chapman, Karen B.

; APPLICANT: Morin, Gregg B.

; APPLICANT: Harley, Calvin B.

; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 727

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,549A  
; FILING DATE: 19-NOV-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 638:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3396 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 1..3396  
; OTHER INFORMATION: /note= "hTERT-encoding sequence employing  
; OTHER INFORMATION: alternative codon distributions for  
; OTHER INFORMATION: E. coli (all genes)"  
US-08-974-549A-638

## Alignment Scores:

Pred. No.:	8,97e-259	Length:	3396
Score:	4900.00	Matches:	927
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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	97.65%	Indels:	0
DB:	3	Gaps:	0

US-08-951-733-14 (1-949) x US-08-974-549A-638 (1-3396)







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Db 2401 GCTTCTCCGGTCTGTTCGACGTTTCTCTGCGTTTTCATGTGCACACGCTGTTGATC 2460  
Qy 843 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 862  
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Db 2521 CTGTGCTCCCTGTCTACGGTGACATGGAACAACTGTTGCTGGTATCGTGTGAC 2580  
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Qy 923 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 942  
Db 2701 CETAACCGTGTGTTAACTCCCGCTTGAAGACGAAGCTCTGGTGGTACCGCTTTCGTT 2760  
Qy 943 GlnMetProAlaHisGlyLeu 949  
Db 2761 CAGATGCCGGCTCACGGTCTG 2781

RESULT 14

US-08-974-549A-640  
; Sequence 640, Application US/08974549A  
; Patent No. 6166178  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin B.  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,549A  
; FILING DATE: 19-NOV-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-0026100S  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 640:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3396 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 1..3396  
; OTHER INFORMATION: /note= "hTERT-encoding sequence employing  
; OTHER INFORMATION: alternative codon distributions for  
; OTHER INFORMATION: yeast (all genes)"  
US-08-974-549A-640

Alignment Scores:  
Pred. No.: 8,97e-259 Length: 3396  
Score: 4900.00 Matches: 927  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 97.65% Indels: 0  
DB: 3 Gaps: 0  
US-08-951-733-14 (1-949) x US-08-974-549A-640 (1-3396)  
Qy 23 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 42  
Db 1 ATGCCAAGAGCTCCCAAGATGTAGAGCTGTAGATCTTTTGTGAGATCTCATTTATAGAGAA 60  
Qy 43 ValLeuProLeuAlaThrPheValArgLeuGlyProGlnGlyTrpArgLeuValGln 62  
Db 61 GTTTTGCCATTGGCTACTTTTGTAGAGATTGGGTCCACAAGGTTGGAGATTGGTTCAA 120  
Qy 63 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValProTrp 82  
Db 121 AGAGGTGATCCAGCTGCTTTTAGAGCTTTGGTGTGCTCATATGTTGGTTGTCTCCATGG 180  
Qy 83 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 102  
Db 181 GATGCTAGACCAACCACCACTGCTCCATCTTTTAGACAAGATTCTTGTGTTGAAGAAGATTG 240  
Qy 103 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 122  
Db 241 GTTGTAGAGTTTGCAAAGATTGTGTGAAGAGGTGCTGTAAGAGGTTGTTTGGCTTTTGGT 300  
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QY 923 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 942  
Db 2701 AGAAAACTGTTGTTAAATTTCCAGCTTGAAGATGAAGCTTTTGGTGGTACTGCTTTGTT 2760  
QY 943 GlnMetProAlaHisGlyLeu 949  
Db 2761 CAAATGCCAGCTCATGTTTG 2781

## RESULT 15

US-08-974-549A-641  
; Sequence 641, Application US/08974549A  
; Patent No. 6166178  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin B.  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF INVENTIONS: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,549A  
; FILING DATE: 19-NOV-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; PRIOR APPLICATION DATA:  
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; FILING DATE: 18-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
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; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-0026100S  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 641:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3396 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 1..3396  
; OTHER INFORMATION: /note= "hTERT-encoding sequence employing  
; OTHER INFORMATION: alternative codon distributions for  
; OTHER INFORMATION: yeast (high expressing genes)"  
US-08-974-549A-641

## Alignment Scores:

Pred. No.: 8 97e-259 Length: 3396  
Score: 4900.00 Matches: 927  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 97.65% Indels: 0  
DB: 3 Gaps: 0

US-08-951-733-14 (1-949) x US-08-974-549A-641 (1-3396)

QY 23 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 42  
Db 1 ATGCCAAGAGCTCCCAAGATGTAGAGCTTTAGATCTTTTGGATCTCTCACTACAGAGAA 60  
QY 43 ValLeuProLeuAlaThrPheValArgLeuGlyProGlnGlyTrpArgLeuValGln 62  
Db 61 GTTTTGCCATTCGCTACTTTTCGTAGAGATTGGGTCACAAAGTTGGAGATTGGTTCAA 120  
QY 63 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 82  
Db 121 AGAGGTGACCCAGCTGCTTCAGAGCTTTGGTTGCTCAATGTTGGTTTGTCTCCATGG 180  
QY 83 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 102  
Db 181 GACGCTAGACCACACCAGCTGCTCCATCTTTTCAGACAAAGTTTCTTTGTTGAAGGAATTC 240  
QY 103 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 122  
Db 241 GTTGCTAGAGTTTTCGAAGATTGTGTGAAGAGGTGCTTAAGAACGTTTGGCTTCGGT 300  
QY 123 PheAlaLeuLeuAspGlyAlaAlaArgGlyGlyProProGluAlaPheThrThrSerValArg 142  
Db 301 TTCGCTTTGTTGGACGGTGTAGAGGTGGTCCACAGAGCTTTCACTACTCTCTGTAGA 360  
QY 143 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu 162  
Db 361 TCTTACTTCCCAACACACTGTTACTACGCTTTTGGAGAGGTTCTGGTCTGGGGTTGTTG 420  
QY 163 LeuArgArgValGlyAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 182  
Db 421 TTGAGAAGAGTTGGTGACGACGCTTTGGTTGCTACTTTGTTGGCTAGATGCTGTTGCGTT 480  
QY 183 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 202  
Db 481 TTGGTTGCTCCATCTTGTGCTTACCAAGTTTGTGGTCCACCATTGTACCAATTGGTGCT 540





Db 2701 AGAAGACTGTGTAACTTCCAGTTGAGAGACGAAGCTTTGGTGGTACTGCTTCGTT 2760

Qy 943 GlnMetProAlaHisGlyLeu 949

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Copyright (c) 1993 - 2003 Compugen Ltd.

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Searched: 569978 seqs, 220691566 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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14	898.4	99.7	4029	3	US-08-854-050-173
15	898.4	99.7	4029	4	US-09-430-323-173
16	597.6	66.3	3451	3	US-08-974-549A-721
17	591.2	65.6	3396	3	US-08-974-549A-639
18	581.8	64.6	3396	3	US-08-974-549A-638
19	537	58.5	2176	3	US-08-974-549A-3
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21	527	58.5	3855	3	US-08-974-549A-4
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28	469.6	52.1	3396	3	US-08-974-549A-641	Sequence 641, App
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30	186.8	20.7	51552	4	US-09-733-294A-30	Sequence 30, Appl
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33	161	17.9	409	4	US-09-733-294A-31	Sequence 31, Appl
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37	159	17.6	389	4	US-09-430-323-62	Sequence 8, Appl1
38	159	17.6	389	4	US-08-912-951-8	Sequence 8, Appl1
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42	65	7.2	90	3	US-08-974-549A-690	Sequence 690, App
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#### ALIGNMENTS

RESULT 1  
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Patent No. 6093809  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: No. 6093809el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,843A  
FILING DATE: 06-MAY-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 224:

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "hrrr"
; OTHER INFORMATION: /note= "human telomerase reverse
; OTHER INFORMATION: transcriptase (hrrr) catalytic protein
; OTHER INFORMATION: component"
;
US-08-851-843A-224

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Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 GGCCAGAGCCGCGGCTGAGCTGTACTTTGCAAGGTGATGTGACGGCGGTACGA 300
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## RESULT 2

US-08-974-549A-1

; Sequence 1, Application US/08974549A

; Patent No. 6166178

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; APPLICANT: Lingner, Joachim

; APPLICANT: Nakamura, Toru

; APPLICANT: Chapman, Karen B.

; APPLICANT: Morin, Gregg B.

; APPLICANT: Harley, Calvin B.

; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 727

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/974,549A

; FILING DATE: 19-NOV-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/911,312

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/912,951

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

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; FILING DATE: 14-AUG-1997

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; FILING DATE: 01-OCT-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/17885

; FILING DATE: 01-OCT-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph Ted

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/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002610US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4015 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
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/ OTHER INFORMATION: /product= "hprt"
/ OTHER INFORMATION: /note= "human telomerase reverse
/ OTHER INFORMATION: transcriptase (hTERT) catalytic protein
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Query Match 100.0%; Score 901; DB 3; Length 4015;
Best Local Similarity 100.0%; Pred. No. 3.9e-210;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2809 T 2809

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; Sequence 224, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 224:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
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; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "htrrt"
; OTHER INFORMATION: /note= "human telomerase reverse
; OTHER INFORMATION: transcriptase (htrrt) catalytic protein
; OTHER INFORMATION: component"
; US-08-854-050-224

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Best Local Similarity 100.0%; Pred. No. 3.9e-210;
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 224, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 224:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "htrrt"
; /note= "human telomerase reverse
; transcriptase (htrrt) catalytic protein
; component"
; SEQUENCE DESCRIPTION: SEQ ID NO: 224:
; US-09-430-323-224
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Query Match 100.0%; Score 901; DB 4; Length 4015;  
Best Local Similarity 100.0%; Pred. No. 3.9e-210;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1969 CGTCGTGGAGCCAGAACGTTCCGAGAGAAAGAGGGCGGCGTCTCACCTCGAGGGT 2028  
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RESULT 5  
US-09-572-423B-3  
; Sequence 3, Application US/09572423B

Patent No. 6331399  
GENERAL INFORMATION:  
APPLICANT: Brett P. Monia  
APPLICANT: William A. Gaarde  
APPLICANT: Edward Wanciewicz  
TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION  
FILE REFERENCE: TSPH-0462  
CURRENT APPLICATION NUMBER: US/09/572,423B  
CURRENT FILING DATE: 2000-05-16  
NUMBER OF SEQ ID NOS: 29  
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LENGTH: 4015  
TYPE: DNA  
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LOCATION: (56)...(3454)  
US-09-572-423B-3

Query Match 100.0%; Score 901; DB 4; Length 4015;  
Best Local Similarity 100.0%; Pred. No. 3.9e-210;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 781 CCACGGGAAAACCTTCTCAGAGACCTGTGTCGAGGTGTCCTGTAGTATGGTGGTGT 840  
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QY 841 GAACTTGGGAGACAGTGTGAACCTTCCCTGTAGAAGACGAGGCGCTGGTGGCAGGC 900  
DB 2749 GAACTTGGGAGACAGTGTGAACCTTCCCTGTAGAAGACGAGGCGCTGGTGGCAGGC 2808  
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DB 2809 T 2809

Db 2629 GCGGACGGGCTGCTCTCGCGCTTTGGTGGATGAATTCCTTTGTTGGTGACACCTCACTCTCAC 2688  
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Db 2689 CCACGCGAAAACTTCCTCAGGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGGTGGT 2748  
QY 841 GAACCTGGGGAAGACAGTGGTGAACCTCCCTGTGAGAACAGAGGCCCTGGGTGGGACGGC 900  
Db 2749 GAACCTGGGGAAGACAGTGGTGAACCTCCCTGTGAGAACAGAGGCCCTGGGTGGGACGGC 2808  
QY 901 T 901  
Db 2809 T 2809

RESULT 6  
US-09-128-354-1  
; Sequence 1, Application US/09128354  
; Patent No. 6337200  
; GENERAL INFORMATION:  
; APPLICANT: Morin, Gregg B.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants  
; FILE REFERENCE: 015389-003310US  
; CURRENT APPLICATION NUMBER: US/09/128,354  
; CURRENT FILING DATE: 1998-08-03  
; EARLIER APPLICATION NUMBER: US 08/851,843  
; EARLIER FILING DATE: 1997-05-06  
; EARLIER APPLICATION NUMBER: US 08/854,050  
; EARLIER FILING DATE: 1997-05-09  
; EARLIER APPLICATION NUMBER: US 08/911,312  
; EARLIER FILING DATE: 1997-08-14  
; EARLIER APPLICATION NUMBER: US 08/912,951  
; EARLIER FILING DATE: 1997-08-14  
; EARLIER APPLICATION NUMBER: US 08/915,503  
; EARLIER FILING DATE: 1997-08-14  
; EARLIER APPLICATION NUMBER: WO PCT/US97/17618  
; EARLIER FILING DATE: 1997-10-01  
; EARLIER APPLICATION NUMBER: WO PCT/US97/17885  
; EARLIER FILING DATE: 1997-10-01  
; EARLIER APPLICATION NUMBER: US 08/974,549  
; EARLIER FILING DATE: 1997-11-19  
; EARLIER APPLICATION NUMBER: US 08/974,584  
; EARLIER FILING DATE: 1997-11-19  
; EARLIER APPLICATION NUMBER: US 09/052,864  
; EARLIER FILING DATE: 1998-03-31  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4015  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (56)..(3454)  
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cdNA  
US-09-128-354-1

Query Match 100.0%; Score 901; DB 4; Length 4015;  
Best Local Similarity 100.0%; Pred. No. 3.9e-210;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTCCAGACTCGGCTTCATCCCAAGCCTGACGGGCTCGCGCCGATTCTGAACATGGACTA 60  
Db 1909 GTCCAGACTCGGCTTCATCCCAAGCCTGACGGGCTCGCGCCGATTCTGAACATGGACTA 1968  
QY 61 CGTCGTGGGAGCCAGAACAGTTCGCGAGAGAAAAGAGGCCCGAGCGTCTCACCTCGAGGGT 120  
Db 1969 CGTCGTGGGAGCCAGAACAGTTCGCGAGAGAAAAGAGGCCCGAGCGTCTCACCTCGAGGGT 2028  
QY 121 GAAGGCACTGTTGAGCGGTGCTCACTACGAGCGGGCGGGCGGCTCTCTGGGCGC 180  
Db 2029 GAAGGCACTGTTGAGCGGTGCTCACTACGAGCGGGCGGGCGGCTCTCTGGGCGC 2088

QY 181 CTCCTGCTGGSCCTGGACGATATCCACAGGSCCTGGGCGACCTTCCTGCTCGCTGGTGGC 240  
Db 2089 CTCCTGCTGGSCCTGGACGATATCCACAGGSCCTGGGCGACCTTCCTGCTCGCTGGTGGC 2148  
QY 241 GGGCCAGGACCGCGCCCTGAGCTGCTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGA 300  
Db 2149 GGGCCAGGACCGCGCCCTGAGCTGCTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGA 2208  
QY 301 CACCATCCCGCAGGACAGGCTCACGGAGGTGTCATCCCGAGCATCATCAAAACCCCAACAC 360  
Db 2209 CACCATCCCGCAGGACAGGCTCACGGAGGTGTCATCCCGAGCATCATCAAAACCCCAACAC 2268  
QY 361 GTACTGCTGGTGTGCTGATGCGGTGCTCAGAAAGCCGCCATGGGCGAGTCCGCAAGGC 420  
Db 2269 GTACTGCTGGTGTGCTGATGCGGTGCTCAGAAAGCCGCCATGGGCGAGTCCGCAAGGC 2328  
QY 421 CTTCAAGAGCCACGCTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGC 480  
Db 2329 CTTCAAGAGCCACGCTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGC 2388  
QY 481 TCACCTGAGGAGACAGCCGCGCTGAGGATGCCGTGCTCATCGAGCAGAGTCTCTCCCT 540  
Db 2389 TCACCTGAGGAGACAGCCGCGCTGAGGATGCCGTGCTCATCGAGCAGAGTCTCTCCCT 2448  
QY 541 GAATGAGGCCAGCAGTGGCTCTTTCGACGTCTTCTACGTCTTATGTGCGACACGCGGT 600  
Db 2449 GAATGAGGCCAGCAGTGGCTCTTTCGACGTCTTCTACGTCTTATGTGCGACACGCGGT 2508  
QY 601 GCGCATCAGGGGCAAGTCTCTACGTGACGTGCGAGGGATCCCGAGGCTCCATCTCTC 660  
Db 2509 GCGCATCAGGGGCAAGTCTCTACGTGACGTGCGAGGGATCCCGAGGCTCCATCTCTC 2568  
QY 661 CACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTTGGGGGATTCG 720  
Db 2569 CACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTTGGGGGATTCG 2628  
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Db 2629 GCGGACGCGGTGCTCTCTGCGTTTGGTGGATGATTCTTGTGGTGACACCTCACTCAC 2688  
QY 781 CCACGCGAAAACCTTCCTCAGGACCCCTGGTCCGAGGTGTCCTGATAGTATGGTGGTGGT 840  
Db 2689 CCACGCGAAAACCTTCCTCAGGACCCCTGGTCCGAGGTGTCCTGATAGTATGGTGGTGGT 2748  
QY 841 GAACCTGCGGAAGACAGTGGTGAACCTCCCTGTGAGAACAGAGGCCCTGGGTGGGACGGC 900  
Db 2749 GAACCTGCGGAAGACAGTGGTGAACCTCCCTGTGAGAACAGAGGCCCTGGGTGGGACGGC 2808  
QY 901 T 901  
Db 2809 T 2809

RESULT 7  
US-09-675-321-1  
; Sequence 1, Application US/09675321  
; Patent No. 6440735  
; GENERAL INFORMATION:  
; APPLICANT: Gaeta, Federico C.A.  
; APPLICANT: Geron Corporation  
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune  
; FILE REFERENCE: 015389-003500PC  
; CURRENT APPLICATION NUMBER: US/09/675,321  
; CURRENT FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/112,006  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898  
; PRIOR FILING DATE: 1999-03-30  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1

;< br>LENGTH: 4015< br>TYPE: DNA< br>ORGANISM: Homo sapiens< br>FEATURE:< br>NAME/KEY: CDS< br>LOCATION: (36)..(3454)< br>OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)< br>US-09-675-321-1

Query Match 100.0%; Score 901; DB 4; Length 4015;

Best Local Similarity 100.0%; Pred. No. 3.9e-210;

Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGCTGCGCGGATGTGAACATGACATA 60

DB 1909 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGCTGCGCGGATGTGAACATGACATA 1968

QY 61 CGTCGTGGAGCCAGAACCTTCGCGAGAGAAAGAGCGCTCTCACCTCGAGGGT 120

DB 1969 CGTCGTGGAGCCAGAACCTTCGCGAGAGAAAGAGCGCTCTCACCTCGAGGGT 2028

QY 121 GAAGGCATGTTCAAGCTGCTCAACTACAGGGGGCGGGCCCGGGCTCTCTGGCGGC 180

DB 2029 GAAGGCATGTTCAAGCTGCTCAACTACAGGGGGCGGGCCCGGGCTCTCTGGCGGC 2088

QY 181 CTCGTGTCTGGCGCTGGAGCATATCCACAGGGCCTGGCGCACTTCGTGCTGCTGTGCG 240

DB 2089 CTCGTGTCTGGCGCTGGAGCATATCCACAGGGCCTGGCGCACTTCGTGCTGCTGTGCG 2148

QY 241 GSCCCAGGACCCCGCCCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGGCGGTACGA 300

DB 2149 GSCCCAGGACCCCGCCCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGGCGGTACGA 2208

QY 301 CACCATCCCCAGGACAGGCTCAGGAGTCAATCGCCAGCATCATCAAAACCCAGAACAC 360

DB 2209 CACCATCCCCAGGACAGGCTCAGGAGTCAATCGCCAGCATCATCAAAACCCAGAACAC 2268

QY 361 GTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

DB 2269 GTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2328

QY 421 CTTCAAGACCCACGCTCTTACCTTGACAGACCTCCAGCCGTACATCGGACAGTTCGTGGC 480

DB 2329 CTTCAAGACCCACGCTCTTACCTTGACAGACCTCCAGCCGTACATCGGACAGTTCGTGGC 2388

QY 481 TCACCTCAGGACAGACGCCCCGCTGAGGATGCGCTGCTCATCGAGCAGAGTCTCTCCCT 540

DB 2389 TCACCTCAGGACAGACGCCCCGCTGAGGATGCGCTGCTCATCGAGCAGAGTCTCTCCCT 2448

QY 541 GAATGAGGCCAGCAGTGGCTCTTCGACGCTTCCTACGCTTCATGTCGACACGCGCT 600

DB 2449 GAATGAGGCCAGCAGTGGCTCTTCGACGCTTCCTACGCTTCATGTCGACACGCGCT 2508

QY 601 GCGCATCAGGGGCAAGTCTTACGTCAGTGCAGGGGATCCGCGAGGGTCCATCTCTCTC 660

DB 2509 GCGCATCAGGGGCAAGTCTTACGTCAGTGCAGGGGATCCGCGAGGGTCCATCTCTCTC 2568

QY 661 CAGCTGCTCTCGACGCTGCTACGGGACATGAGAACAGCTGTTTCGGGGGATTCG 720

DB 2569 CAGCTGCTCTCGACGCTGCTACGGGACATGAGAACAGCTGTTTCGGGGGATTCG 2628

QY 721 GCGGACGGGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

DB 2629 GCGGACGGGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2688

QY 781 CCACGCGAAACCTTCTCAGGACCTTGCTCGAGGTGTCCTTGAGTATGGCTGCTGCTG 840

DB 2689 CCACGCGAAACCTTCTCAGGACCTTGCTCGAGGTGTCCTTGAGTATGGCTGCTGCTG 2748

QY 841 GAACCTGCGGAAGACAGTGGTGAATTCCTCTAGAACAGAGGCCCTGGGTGGCACGGC 900

DB 2749 GAACCTGCGGAAGACAGTGGTGAATTCCTCTAGAACAGAGGCCCTGGGTGGCACGGC 2808

QY 901 T 901< br>DB 2809 T 2809

# RESULT 8

US-09-052-919-1

; Sequence 1, Application US/09052919

; Patent No. 6444650

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; APPLICANT: Lingner, Joachim

; APPLICANT: Nakamura, Toru

; APPLICANT: Chapman, Karen B.

; APPLICANT: Morin, Gregg B.

; APPLICANT: Harley, Calvin B.

; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: Antisense Compositions for Detecting and

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/052,919

; FILING DATE: 31-MAR-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 23-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/911,312

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/912,951

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/915,503

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/974,549

; FILING DATE: 19-NOV-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/974,584

; FILING DATE: 19-NOV-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/17618

; FILING DATE: 01-OCT-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/17885

; FILING DATE: 01-OCT-1997

; ATTORNEY/AGENT INFORMATION:

NAME: Parent, Annette S.  
REGISTRATION NUMBER: 42,058  
REFERENCE/DOCKET NUMBER: 015389-003600US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4015 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 56..3454  
OTHER INFORMATION: /product= "human telomerase reverse transcriptase (hTERT)"  
US-09-052-919-1  
Query Match 100.0%; Score 901; DB 4; Length 4015;  
Best Local Similarity 100.0%; Pred. No. 3.9e-210; Indels 0; Gaps 0;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTCAGACTCGGCTTCATCCCAAGCTGAGGGCTGGGCGGATTTGGAACATGGACTA 60  
Db 1909 GTCCAGACTCGGCTTCATCCCAAGCTGAGGGCTGGGCGGATTTGGAACATGGACTA 1968  
Qy 61 CGTCGTGGGAGCAGAGCTTCCGACAGAAAGAGGCGGAGCTCTACCTCGAGGGT 120  
Db 1969 CGTCGTGGGAGCAGAGCTTCCGACAGAAAGAGGCGGAGCTCTACCTCGAGGGT 2028  
Qy 121 GAAGGCACTGTTACAGCTGTCTCAACTACGAGCGGCGGCGCCCGCTCTCTGGGCGC 180  
Db 2029 GAAGGCACTGTTACAGCTGTCTCAACTACGAGCGGCGGCGCCCGCTCTCTGGGCGC 2088  
Qy 181 CTCGTGCTGGGCTTGACAGATATCCACAGGGCTGGGCGGAGCTCTGCTGTGCTGG 240  
Db 2089 CTCGTGCTGGGCTTGACAGATATCCACAGGGCTGGGCGGAGCTCTGCTGTGCTGG 2148  
Qy 241 GGCCAGAGCCGCGCTGAGCTGTACTTTGCAAGTGTGATGTGAGCGGCGGTACGA 300  
Db 2149 GGCCAGAGCCGCGCTGAGCTGTACTTTGCAAGTGTGATGTGAGCGGCGGTACGA 2208  
Qy 301 CACATCCCCAGACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGAACAC 360  
Db 2209 CACATCCCCAGACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGAACAC 2268  
Qy 361 GTACTGCGTGGCTGATGCGGTGTCAGAGCTTCCAGAGCGGCGGATGCGCAAGGC 420  
Db 2269 GTACTGCGTGGCTGATGCGGTGTCAGAGCTTCCAGAGCGGCGGATGCGCAAGGC 2328  
Qy 421 CTTCAAGAGCAGCTCTACCTTTGACAGACCTCCAGCGGTACATGCGAGCTTCGTGGC 480  
Db 2329 CTTCAAGAGCAGCTCTACCTTTGACAGACCTCCAGCGGTACATGCGAGCTTCGTGGC 2388  
Qy 481 TCACCTGCAGGAGACCCCGCTGAGGGATCGCGTCTCATCGAGCAGAGCTCCTCCCT 540  
Db 2389 TCACCTGCAGGAGACCCCGCTGAGGGATCGCGTCTCATCGAGCAGAGCTCCTCCCT 2448  
Qy 541 GAATGAGGCGAGAGTGGCTCTTCGAGCTTCTCCTAGCTTCTATGTCACACAGCGGT 600  
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Db 2569 CACGCTCTGCGAGCTGTGCTACGCGGACATGGAGAACAGCTGTTTGGGGGATTCG 2628  
Qy 721 GCGGAGCGGGCTGCTCTCGGTTTGGTGGATGATTTCTTGTGAGACCTCACCTCAC 780

Db 2629 GCGGAGCGGGCTGCTCTCGGTTTGGTGGATGATTTCTTGTGAGACCTCACCTCAC 2688  
Qy 781 CCACGCGAAAACCTTCTCCAGGACCTGCTCCGAGGTGCTCCCTGAGTATGCTGGTGGT 840  
Db 2689 CCACGCGAAAACCTTCTCCAGGACCTGCTCCGAGGTGCTCCCTGAGTATGCTGGTGGT 2748  
Qy 841 GAACCTGCGGAAGACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCGCTGGGTGGCAGCGC 900  
Db 2749 GAACCTGCGGAAGACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCGCTGGGTGGCAGCGC 2808  
Qy 901 T 901  
Db 2809 T 2809  
RESULT 9  
US-08-912-951-1  
; Sequence 1, Application US/08912951  
; Patent No. 6475789  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND  
; NUMBER OF SEQUENCES: 335  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912,951  
; FILING DATE: 14-AUG-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002600US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4015 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 56..3454  
; OTHER INFORMATION: /product= "hTERT"  
; /note= "human telomerase reverse  
; OTHER INFORMATION: transcriptase (hTERT) catalytic protein  
; OTHER INFORMATION: component"  
US-08-912-951-1

Query Match 100.0%; Score 901; DB 4; Length 4015;  
Best Local Similarity 100.0%; Pred. No. 3.9e-210;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGGCTCGCGCGATGTGAACATGACTA 60  
Db 1909 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGGCTCGCGCGATGTGAACATGACTA 1968  
QY 61 CTTCTGTGGAGCCAGAGAGTCCCGAGAGAAAGAGGCGCCGAGCGCTCACCTCAGGGT 120  
Db 1969 CTTCTGTGGAGCCAGAGAGTCCCGAGAGAAAGAGGCGCCGAGCGCTCACCTCAGGGT 2028  
QY 121 GAAGGCACTGTTACGCTGCTCACTACGAGCGGCGCGCGCCGCTCCTGGGCGC 180  
Db 2029 GAAGGCACTGTTACGCTGCTCACTACGAGCGGCGCGCGCCGCTCCTGGGCGC 2088  
QY 181 CTCTGTGTGGGCTTGGAGCATATCCACAGGCGCTTGGCGCACCTTCTGCTGCGTGTGCG 240  
Db 2089 CTCTGTGTGGGCTTGGAGCATATCCACAGGCGCTTGGCGCACCTTCTGCTGCGTGTGCG 2148  
QY 241 GSCCAGAGCCGCGCGCTGAGCTGCTACTTTGTCAAGTGGATGTGAGGGCGGTACGA 300  
Db 2149 GSCCAGAGCCGCGCGCTGAGCTGCTACTTTGTCAAGTGGATGTGAGGGCGGTACGA 2208  
QY 301 CACCATCCCGAGGACAGGCTCACGAGGTCTATCCGACAGCATCATCAAAACCCAGAACAC 360  
Db 2209 CACCATCCCGAGGACAGGCTCACGAGGTCTATCCGACAGCATCATCAAAACCCAGAACAC 2268  
QY 361 GTACTGCTGCTGCGTATGCGGTTCAGAGGCCGCCATGGGCGACGTCGCGCAAGGC 420  
Db 2269 GTACTGCTGCTGCGTATGCGGTTCAGAGGCCGCCATGGGCGACGTCGCGCAAGGC 2328  
QY 421 CTTCAAGAGCCACGCTCTACTTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGGC 480  
Db 2329 CTTCAAGAGCCACGCTCTACTTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGGC 2388  
QY 481 TCACCTGACGAGACAGCCGCTGAGGATGCCGCTGCTCATCGAGCAGAGCTCTCCCT 540  
Db 2389 TCACCTGACGAGACAGCCGCTGAGGATGCCGCTGCTCATCGAGCAGAGCTCTCCCT 2448  
QY 541 GAATGAGCCAGCAGTGGCTTCGAGCGTCTTCCATGCTTCACTGCTTCATGTCGACAGCCGT 600  
Db 2449 GAATGAGCCAGCAGTGGCTTCGAGCGTCTTCCATGCTTCACTGCTTCATGTCGACAGCCGT 2508  
QY 601 GCGCATAGGGGCAAGTCTACGTCCAGTCCAGGGGATCCGAGGGCTCCATCTCTC 660  
Db 2509 GCGCATAGGGGCAAGTCTACGTCCAGTCCAGGGGATCCGAGGGCTCCATCTCTC 2568  
QY 661 CACGCTGCTCTGACGCTGTGTACGGCGACATGAGAACAGCTGTTTGGGGGATTCG 720  
Db 2569 CACGCTGCTCTGACGCTGTGTACGGCGACATGAGAACAGCTGTTTGGGGGATTCG 2628  
QY 721 GCGGACCGGGCTGCTCTCGGTTTGGTGATGATTTCTTGTGTTGACACCTTCACCTCAC 780  
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QY 781 CCACGCGAAACCTTCCTCAGAACCCCTGGTCCGAGGTGCTCCCTGAGTATGGCTGCGTGGT 840  
Db 2689 CCACGCGAAACCTTCCTCAGAACCCCTGGTCCGAGGTGCTCCCTGAGTATGGCTGCGTGGT 2748  
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QY 901 T 901  
Db 2809 T 2809

RESULT 10  
US-09-733-294A-3  
; Sequence 3, Application US/09733294A  
; Patent No. 6492171  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: William Gaarde  
; APPLICANT: Susan M. Freier  
; APPLICANT: Edward V. Wanciewicz  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION  
; FILE REFERENCE: ISPH-0527  
; CURRENT APPLICATION NUMBER: US/09/733,294A  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: 09/572,423  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 108  
; SEQ ID NO 3  
; LENGTH: 4015  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (56)...(3454)  
US-09-733-294A-3

Query Match 100.0%; Score 901; DB 4; Length 4015;  
Best Local Similarity 100.0%; Pred. No. 3.9e-210;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGGCTCGCGCGATGTGAACATGACTA 60  
Db 1909 GTCCAGACTCCGCTTCATCCCAAGCCTGACGGGCTCGCGCGATGTGAACATGACTA 1968  
QY 61 CTTCTGTGGAGCCAGAGAGTTCCTCCGAGAGAAAGAGGCGCCGAGCGCTCACCTCAGGGT 120  
Db 1969 CTTCTGTGGAGCCAGAGAGTTCCTCCGAGAGAAAGAGGCGCCGAGCGCTCACCTCAGGGT 2028  
QY 121 GAAGGCACTGTTACGCTGCTCACTACGAGCGGCGCGCGCCGCTCCTGGGCGC 180  
Db 2029 GAAGGCACTGTTACGCTGCTCACTACGAGCGGCGCGCGCCGCTCCTGGGCGC 2088  
QY 181 CTCTGTGTGGGCTTGGAGCATATCCACAGGCGCTTGGCGCACCTTCTGCTGCGTGTGCG 240  
Db 2089 CTCTGTGTGGGCTTGGAGCATATCCACAGGCGCTTGGCGCACCTTCTGCTGCGTGTGCG 2148  
QY 241 GSCCAGAGCCGCGCGCTGAGCTGCTACTTTGTCAAGTGGATGTGAGGGCGGTACGA 300  
Db 2149 GSCCAGAGCCGCGCGCTGAGCTGCTACTTTGTCAAGTGGATGTGAGGGCGGTACGA 2208  
QY 301 CACCATCCCGAGGACAGGCTCACGAGGTCTATCCGACAGCATCATCAAAACCCAGAACAC 360  
Db 2209 CACCATCCCGAGGACAGGCTCACGAGGTCTATCCGACAGCATCATCAAAACCCAGAACAC 2268  
QY 361 GTACTGCTGCTGCGTATGCGGTTCAGAGGCCGCCATGGGCGACGTCGCGCAAGGC 420  
Db 2269 GTACTGCTGCTGCGTATGCGGTTCAGAGGCCGCCATGGGCGACGTCGCGCAAGGC 2328  
QY 421 CTTCAAGAGCCACGCTCTACTTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGGC 480  
Db 2329 CTTCAAGAGCCACGCTCTACTTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGGC 2388

QY 481 TCACCTGCAGGACGACCGCGCTGAGGATGCCGCTCATCGACGAGCTCCTCCCT 540  
Db 2389 TCACCTGCAGGACGACCGCGCTGAGGATGCCGCTCATCGACGAGCTCCTCCCT 2448  
QY 541 GAATGAGCGACGAGTGGCTCTTCGACGCTTCTTACGCTTTCATGTCACACGCGGT 600  
Db 2449 GAATGAGCGACGAGTGGCTCTTCGACGCTTCTTACGCTTTCATGTCACACGCGGT 2508  
QY 601 GCCATCAGGGGCAAGCTTCTACGCTCAGTCGACGAGGATCCCGCAGGGCTCCTATCTCTC 660  
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QY 661 CACGCTGCTCAGGCTGTCTACGCGGACATGAGAACAACTGTTTGGGGGATTCG 720  
Db 2569 CACGCTGCTCAGGCTGTCTACGCGGACATGAGAACAACTGTTTGGGGGATTCG 2628  
QY 721 CGCGGAGGCGCTCCTCGCTTGTGGTGGATGTTTCTTGGTGACACCTCACCTCAC 780  
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QY 781 CCACGCGAAACCTTCTCAGGACCTGTCAGGCTGTCGAGGTGCTCCCTGAGTATGGCTGCTG 840  
Db 2689 CCACGCGAAACCTTCTCAGGACCTGTCAGGCTGTCGAGGTGCTCCCTGAGTATGGCTGCTG 2748  
QY 841 GAATTCGCGAAGACAGTGTGTAACCTTCCCTGTAGAGACGAGGCGCTGGTGGCACGGC 900  
Db 2749 GAATTCGCGAAGACAGTGTGTAACCTTCCCTGTAGAGACGAGGCGCTGGTGGCACGGC 2808  
QY 901 T 901  
Db 2809 T 2809

RESULT 11

US-08-974-549A-343  
; Sequence 343, Application US/08974549A  
; Patent No. 6166178

GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin B.  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 19-NOV-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 343:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4037 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 56..3454  
; OTHER INFORMATION: /note= "refined sequence of hTERT cDNA"  
US-08-974-549A-343

Query Match 100.0%; Score 901; DB 3; Length 4037;  
Best Local Similarity 100.0%; Pred. No. 3.9e-210;  
Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCAGACTCCGCTTTCATCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGGACTA 60  
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QY 61 CGTCGTGGGAGCCAGAACAGTTCGCGAGAGAAAAGAGGCGGCGAGCGTCTCACCTCGAGGGT 120  
Db 1969 CGTCGTGGGAGCCAGAACAGTTCGCGAGAGAAAAGAGGCGGCGAGCGTCTCACCTCGAGGGT 2028  
QY 121 GAAGGCACCTGTTTCAGCGTGTCTCAACTACGAGCGGCGGCGGCCGCCGCTCTCTGGGCGC 180  
Db 2029 GAAGGCACCTGTTTCAGCGTGTCTCAACTACGAGCGGCGGCGGCCGCCGCTCTCTGGGCGC 2088  
QY 181 CTCTGTGCTGGGCTTGACGATATCCACAGGGGCTGGCGCACCTTGTGTGCTGTGGG 240  
Db 2089 CTCTGTGCTGGGCTTGACGATATCCACAGGGGCTGGCGCACCTTGTGTGCTGTGGG 2148  
QY 241 GGCCAGAGCCCGCGCCTGAGCTGTACTTGTCAAGGTGGATGTGACGGGCGCGTACGA 300  
Db 2149 GGCCAGAGCCCGCGCCTGAGCTGTACTTGTCAAGGTGGATGTGACGGGCGCGTACGA 2208  
QY 301 CACCATCCCCCAGGACAGGCTCACGGAGGTTCATCGCCAGCATCATCAAAACCCAGAACAC 360  
Db 2209 CACCATCCCCCAGGACAGGCTCACGGAGGTTCATCGCCAGCATCATCAAAACCCAGAACAC 2268  
QY 361 GTACTGCGTGGTGGTATGCCGTGTTCCAGAGGCGGCCCGCCATGGGACGTCGCGAAGGC 420  
Db 2269 GTACTGCGTGGTGGTATGCCGTGTTCCAGAGGCGGCCCGCCATGGGACGTCGCGAAGGC 2328

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QY 421 CTTCAAGACCCAGCTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGC 480
Db 2329 CTTCAAGACCCAGCTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGC 2388
QY 481 TCACCTGTCAGGAGACCCAGCTGAGGATGCGCTGTCATCGAGAGAGCTCCTCCCT 540
Db 2389 TCACCTGTCAGGAGACCCAGCTGAGGATGCGCTGTCATCGAGAGAGCTCCTCCCT 2448
QY 541 GAATGAGCCAGAGTGGCTTTCGACGTCTTCTACGCTTCATGCTTCATGTCGACACCGCT 600
Db 2449 GAATGAGCCAGAGTGGCTTTCGACGTCTTCTACGCTTCATGCTTCATGTCGACACCGCT 2508
QY 601 GCGCATCAGGCGAAGTCTTACGTCAGTGCAGTGCAGGGGATCCGCGAGGCTCCATCCTCTC 660
Db 2509 GCGCATCAGGCGAAGTCTTACGTCAGTGCAGTGCAGGGGATCCGCGAGGCTCCATCCTCTC 2568
QY 661 CACGTGCTCTCAGCCTGTGTACGGGACATGAGAGAACAGCTGTTTGGGGGATTCG 720
Db 2569 CACGTGCTCTCAGCCTGTGTACGGGACATGAGAGAACAGCTGTTTGGGGGATTCG 2628
QY 721 GCGGACGGGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 2629 GCGGACGGGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2688
QY 781 CCACGGGAAACCTTCTCAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 2689 CCACGGGAAACCTTCTCAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2748
QY 841 GAACCTGGGAAAGACAGTGGTGAACCTTCCCTGTAGAGAGAGGCGCTGGTGGGACGCGC 900
Db 2749 GAACCTGGGAAAGACAGTGGTGAACCTTCCCTGTAGAGAGAGGCGCTGGTGGGACGCGC 2808
QY 901 T 901
Db 2809 T 2809
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## RESULT 12

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US-08-851-843A-173
; Sequence 173, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
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; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0029300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 173:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4029 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..4029
; OTHER INFORMATION: /note= "preliminary sequence for
; OTHER INFORMATION: human TRT cDNA insert of
; OTHER INFORMATION: plasmid pGRN121"
; US-08-851-843A-173
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Query Match 99.7%; Score 898.4; DB 3; Length 4029;
Best Local Similarity 99.8%; Pred. No. 1.7e-209;
Matches 899; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCCAGACTCCGCTTTCATCCCAAGCCTGACGGGCTGCGGGCGGATGTGAACATGGACTA 60
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QY 61 CGTCGTGGGAGCCAGACAGCTTCCGAGAGAAAGAGGGCCGCTCCTCCCTCGAGGCT 120
Db 1964 CGTCGTGGGAGCCAGACAGCTTCCGAGAGAAAGAGGGCCGCTCCTCCCTCGAGGCT 2023
QY 121 GAAGGCACCTGTTTCAAGCTGCTCAACTACAGAGGGGCGGCGGCGGCGCTCCTGGGCGC 180
Db 2024 GAAGGCACCTGTTTCAAGCTGCTCAACTACAGAGGGGCGGCGGCGGCGCTCCTGGGCGC 2083
QY 181 CTCTGTGTGGGCGCTGGAGCATATCCACAGGGCCCTGGCGACCTTCTGCTGCTGTGGC 240
Db 2084 CTCTGTGTGGGCGCTGGAGCATATCCACAGGGCCCTGGCGACCTTCTGCTGCTGTGGC 2143
QY 241 GCGCCAGGACCCGCGCGCTGAGCTGTTTGTCAAGGTGGATGTGACGGGCGCGTACGA 300
Db 2144 GCGCCAGGACCCGCGCGCTGAGCTGTTTGTCAAGGTGGATGTGACGGGCGCGTACGA 2203
QY 301 CACCATCCCCCAGGACAGGCTCAGCGAGGTCTATCGCAGCATCATCAAAACCCAGAACAC 360
Db 2204 CACCATCCCCCAGGACAGGCTCAGCGAGGTCTATCGCAGCATCATCAAAACCCAGAACAC 2263
QY 361 GTACTGCGTGTGCGTATGCGGTGTCAGAGGCGCGCCCATGGSCAGCTCCGCAAGGC 420
Db 2264 GTACTGCGTGTGCGTATGCGGTGTCAGAGGCGCGCCCATGGSCAGCTCCGCAAGGC 2323
QY 421 CTTCAAGAGCCACAGTCTCTACCTTTCAGACACCTTCAGCCGTCATGCGGACAGTTCGTGGC 480
Db 2324 CTTCAAGAGCCACAGTCTCTACCTTTCAGACACCTTCAGCCGTCATGCGGACAGTTCGTGGC 2383
QY 481 TCACCTGCGAGGAGACAGCCCGCTGAGGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
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Db 2444 GAATGAGCCAGCAGTGGCTCTTTCAGCCTTCTTCTACGCTTCTTCTGCTGCTGCTGCTGCT 2503
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Db 2564 CACCTGCTCTGCAGCTGTGCTACGGCGACATGGAGCAAGCTGTTGGGGGATTCG 2623  
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Db 2624 CGGGAGCGGCTGCTCTCGCTTTGGTGGATGATTTCTTGTGTGACACTCACCTCAC 2683  
Qy 781 CCAGCGCAAACTTCTCAGGACCTTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGT 840  
Db 2684 CCAGCGCAAACTTCTCAGGACCTTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGT 2743  
Qy 841 GAACCTCGGAAGACAGTGTGAACCTCCCTGTAGAGACGAGGCCCTGGTGGCAGGCG 900  
Db 2744 GAACCTCGGAAGACAGTGTGAACCTCCCTGTAGAGACGAGGCCCTGGTGGCAGGCG 2803  
Qy 901 T 901  
Db 2804 T 2804

## RESULT 13

US-08-974-549A-292  
Sequence 292, Application US/08974549A  
Patent No. 6166178  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R. ✓  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin B.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 292:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4029 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..4029  
OTHER INFORMATION: /note= "preliminary sequence for  
human TRT cDNA insert of  
plasmid pGRN121"  
US-08-974-549A-292  
Query Match 99.7%; Score 898.4; DB 3; Length 4029;  
Best Local Similarity 99.8%; Pred. No. 1.7e-209;  
Matches 899; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GTCAGACTCCGCTTATCCCAAGCCTGACGGCTCGGGCCGATTGTGAACATGGACTA 60  
Db 1904 GTCAGACTCCGCTTATCCCAAGCCTGACGGCTCGGGCCGATTGTGAACATGGACTA 1963  
Qy 61 CGTCGTGGGAGCCAGAACGTTCCCGCAGAGAAAGAGGGCGGAGCGTCTACCTCGAGGGT 120  
Db 1964 CGTCGTGGGAGCCAGAACGTTCCCGCAGAGAAAGAGGGCGGAGCGTCTACCTCGAGGGT 2023  
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Qy 241 GGCCAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTAGCGGCGGCTACGA 300  
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Qy 421 CTTCAAGAGCCAGCTCTCTACCTTGACAGACCTCCAGCCGCTACATGCGACAGTTCGTGGC 480  
Db 2324 CTTCAAGAGCCAGCTCTCTACCTTGACAGACCTCCAGCCGCTACATGCGACAGTTCGTGGC 2383  
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DB 2444 GAATGAGGCGCAGTGGCTCTTCGACGCTTCTCCACGCTTCTCATGTGCACACGCCGT 2503  
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DB 2504 GCGCATCAGGGGCAAGTCTTACGTCAGTGCCAGGGGATCCCGCAGGGTCTCCATCTCTC 2563  
QY 661 CAGGCTGCTTCGAGGCTGTCTACGCGGACATGGAGACAAAGCTGTTGCGGGGATTCG 720  
DB 2564 CAGGCTGCTTCGAGGCTGTCTACGCGGACATGGAGACAAAGCTGTTGCGGGGATTCG 2623  
QY 721 GCGGACGCGGCTCTCTCGGTTGGTGATGATTTCTTGTGGTGACACCTTCACTCTAC 780  
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QY 781 CCACGCGAAACCTTCTCAGGACCTGTGTCGAGGTGTCCTTGAGTATGGTGCCTGT 840  
DB 2684 CCACGCGAAACCTTCTCAGGACCTGTGTCGAGGTGTCCTTGAGTATGGTGCCTGT 2743  
QY 841 GAACCTGCGGAAGACAGTGGTGAACCTTCTGTAGAGAGAGGCGCTGGTGGCAGGCG 900  
DB 2744 GAACCTGCGGAAGACAGTGGTGAACCTTCTGTAGAGAGAGGCGCTGGTGGCAGGCG 2803  
QY 901 T 901  
DB 2804 T 2804

RESULT 14  
US-08-854-050-173  
; Sequence 173, Application US/08854050  
; Patent No. 6261836  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: No. 6261836el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/854,050  
; FILING DATE: 09-MAY-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 173:  
; SEQUENCE CHARACTERISTICS:  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY:  
; LOCATION: 1..4029 /note= "preliminary sequence for  
; OTHER INFORMATION: human TRT cDNA insert of  
; OTHER INFORMATION: plasmid pGRN121"  
; US-08-854-050-173

Query Match 99.7%; Score 898.4; DB 3; Length 4029;  
Best Local Similarity 99.8%; Pred. No. 1.7e-209;  
Matches 899; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCCAGACTCCGCTTCATCCCAAGGCTGACGGGCTGCGCGCGATTTGTGAACATGGACTA 60  
DB 1904 GTCCAGACTCCGCTTCATCCCAAGGCTGACGGGCTGCGCGCGATTTGTGAACATGGACTA 1963  
QY 61 CGTGTGGGAGCCAGAACGTTCCGAGAGAAAGAGGGCGGCGGCTCTCACCTCGAGGTT 120  
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Db 2804 T 2804

RESULT 15

US-09-430-323-173  
; Sequence 173, Application US/09430323  
; Patent No. 6309867

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. 6309867el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/430,323  
FILING DATE: 29-Oct-1999  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 173:

SEQUENCE CHARACTERISTICS:

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STRANDEDNESS: single

; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: 1..4029  
; LOCATION: /note- "preliminary sequence for  
; human TRT cDNA insert of  
; plasmid pGRN121"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 173:  
US-09-430-323-173  
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Db 2804 T 2804

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GenCore version 5.1.6  
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Run on: October 7, 2003, 09:31:52 ; Search time 635.99 Seconds  
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Perfect score: 6079

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Ygapop 10.0 , Ygapext 0.5  
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Searched: 1708419 seqs, 1275431651 residues

Total number of hits satisfying chosen parameters: 3416838

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	6057	99.6	4015	10	US-09-990-080-1	Sequence 1, Appli
3	6057	99.6	4015	10	US-09-843-676-224	Sequence 224, App
4	6057	99.6	4015	10	US-09-953-052-1	Sequence 1, Appli
5	6057	99.6	4015	14	US-10-053-758-224	Sequence 224, App
6	6057	99.6	4015	14	US-10-208-243-1	Sequence 1, Appli
7	6057	99.6	4015	14	US-10-054-295-224	Sequence 224, App
8	6057	99.6	4015	14	US-10-054-611-224	Sequence 1, Appli
9	6057	99.6	4015	14	US-10-105-963-1	Sequence 1, Appli
10	6057	99.6	4015	14	US-10-044-692-1	Sequence 1, Appli
11	6057	99.6	4015	14	US-10-044-539-1	Sequence 32, Appli
12	5961	98.1	3396	10	US-09-749-728B-32	Sequence 1, Appli
13	5952	97.9	3453	14	US-10-205-629-1	Sequence 1, Appli
14	5952	97.9	13766	12	US-10-105-616-1	Sequence 1, Appli
15	5925	97.5	8742	12	US-10-105-616-6	Sequence 6, Appli
16	5689.5	93.6	3855	14	US-10-044-692-4	Sequence 4, Appli
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19	5675	93.4	4029	11	US-09-438-486-173	Sequence 173, App
20	5675	93.4	4029	14	US-10-053-758-173	Sequence 173, App
21	5675	93.4	4029	14	US-10-054-295-173	Sequence 173, App
22	5675	93.4	4029	14	US-10-054-611-173	Sequence 173, App
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36	2591.5	42.6	2171	11	US-09-766-253-100	Sequence 100, App
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39	2591.5	42.6	2171	14	US-10-054-295-100	Sequence 100, App
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42	2169.5	35.7	1311	14	US-10-294-778-1	Sequence 1, Appli
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44	901	14.8	519	12	US-10-282-960-2	Sequence 2, Appli
45	646	10.6	389	10	US-09-843-676-62	Sequence 62, Appli

#### ALIGNMENTS

RESULT 1  
US-09-733-294A-3  
; Sequence 3, Application US/09733294A  
; Patent No. US20020045588A1  
; GENERAL INFORMATION:  
; APPLICANT: William Gaarde  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Edward V. Wanciewicz  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION  
; FILE REFERENCE: ISPH-0527  
; CURRENT APPLICATION NUMBER: US/09/733,294A  
; CURRENT FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: 09/572,423  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 108  
; SEQ ID NO 3  
; LENGTH: 4015  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (56)...(3454)  
US-09-733-294A-3

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Pred. No.: 0 Length: 4015  
 Score: 6057.00 Matches: 1150  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.64% Indels: 0  
 DB: 9 Gaps: 0

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QY 785 ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu 804
Db 2342 GTCTCTACCTTGACAGACCTCCAGCGGTATCGTGCACAGTTCGTGCTCACCTGCAGGAG 2401
QY 805 ThrSerProLeuArgAspAlaValValIleGluGlnSerSerLeuAsnGluAlaSer 824
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QY 825 SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly 844
Db 2462 AGTGGCCTCTTCGACCTCTTCCTACGCTTCATGTGCCACACGCGCTGCGCATCAGGGC 2521
QY 845 LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys 864
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QY 865 SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu 884
Db 2582 AGCCTGTGTCAGCGACATGAGAACAGCTGTTGCGGGGATTCGGCGGAGCGGCTG 2641
QY 885 LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr 904
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QY 985 GlyPheLysAlaClyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys 1004
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QY 1005 HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr 1024
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QY 1085 GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLysLeu 1104
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Db 3422 CTGCCCTCAGACTTCAAGACCATCTCTGGAC 3451

RESULT 2
US-09-990-080-1
; Sequence 1, Application US/09990080
; Patent No. US20020102686A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 018/258C
; CURRENT APPLICATION NUMBER: US/09/990,080
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 09/052,864
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTRT) cDNA
US-09-990-080-1

Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 6057.00 Matches: 1150
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.64% Indels: 0
DB: 10 Gaps: 0

US-08-951-733-20 (1-1154) x US-09-990-080-1 (1-4015)
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QY 45 ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64
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Qy 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuLeuArg 164  
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; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "human telomerase reverse
; transcriptase (hTERT)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-953-052-1

Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 6057.00 Matches: 1150
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.64% Indels: 0
DB: 10 Gaps: 0

US-08-951-733-20 (1-1154) x US-09-953-052-1 (1-4015)

QY 5 GlnArgCysValLeuLeuAthrTrpGluAlaLeuAlaProAlaAthrProAlaMetPro 24
DB 2 CAGCGCTGCGTCTCGCAGCCTGGGAAGCCCTGGCCCGGCCACCCCGCGATGCG 61

QY 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44
DB 62 CGCGTCCCCGTCGCGAGCGTGGCGTCCCTGCTGGCGACGCCACTACCGCGAGGTGCTG 121

QY 45 ProLeuAlaThrPheValArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64
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QY 65 AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrrAspAla 84
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QY 205 GlnAlaArgProProHisAlaSerGlyProArgArgLeuGlyCysGluArgAla 224
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DB 662 TGGAAACCATGACGTCAGGGAGCGCGGGTCCCGCTGGGGCTGCCAGCGCGGGTGGCAGG 721

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DB 1562 CTCCTGCTGAGGAGCTGACCTGGAGATGAGCGTGGCGGACTGCGCTGGCTGGCAGG 1621

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1025 LysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis 1044  
3062 AGATCTCTCTGTCAGGGCTACAGGTTTCAGCATGTGTGTGAGCTCCCATTTTCAT 3121  
1045 GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu 1064  
3122 CAGCAAGTTTGAAGAACCACCATTTTCTCGCGGTCTCTGTGACACGGCTCCCTC 3181  
1065 CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla 1084  
3182 TGTACTTCCATCTGAAAGCAAGACGACGGATGTGCTGGGGGCGCAAGGGCGCGC 3241  
1085 GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeu 1104  
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1105 ThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGln 1124  
3302 ACTCGACACGGTGTACCTACGTGCCACTCTCTGGGTCACTCAGGACAGCCAGACGAG 3361  
1125 LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsnProAla 1144  
3362 CTGAGTCGGAAGCTCCGGGGACGACGCTGACTGCCTGGAGCGCGCAGCAACCGGCA 3421  
1145 LeuProSerAspPheLysThrIleLeuAsp 1154  
3422 CTGCCCTCAGACTTCAAGACCATCTCTGGAC 3451

RESULT 5  
US-10-053-758-224  
; Sequence 224, Application US/10053758  
; Publication No. US20030032075A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. US20030032075A1el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/053,758  
; FILING DATE: 18-Jan-2002  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/851,843







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Qy 585 ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer 604  
Db 1742 GTCCGAGACACAGCTTCAAAGACAGGCTCTTTTTCACCGAAGAGTGTCTGGAGC 1801  
Qy 605 LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer 624  
Db 1802 AAGTTCAAAGCATTTGAATACAGACAGCACTTGAAGAGGGTGCAGCTCGGGAGCTGTCG 1861  
Qy 625 GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg 644  
Db 1862 GAAGCAGAGGTGAGGAGCATCGGGAAGCCAGGCGCCGCTGTCAGCTCCAGACTCCGC 1921  
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Db 1922 TTTCATCCCAAGCCTGACGGGCTGGCGCGATTTGTGAACATGACATACGTCGTGGAGCC 1981  
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Db 2162 CCGCCTGAGCTGTACTTGTCAAGGTGGATGTACGCGGCGGTACGACACCATCCGCCAG 2221  
Qy 745 AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg 764  
Db 2222 GACAGGCTCAGGAGGTCAATCGCCAGCATCATCAAAACCCAGAACACGTAATCGGTGCGT 2281  
Qy 765 ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis 784  
Db 2282 CGGTATGCGGTGTCCAGAAGGCGGCCCATGGCAGCTCGCAAGGCCCTTCAAGAGCCAC 2341  
Qy 785 ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu 804  
Db 2342 GTCTCTACCTTGACAGACCTCCAGCGGTACATCGACAGTTCGTGCTCACCTCGCAGGAG 2401  
Qy 805 ThrSerProLeuArgAspAlaValValIleGluLysSerSerSerLeuAsnGluAlaSer 824  
Db 2402 ACCAGCCCGCTGAGGATGCCGTCATCGACAGAGCTCTCTCCCTGATGAGGCAGC 2461  
Qy 825 SerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIleArgGly 844  
Db 2462 AGTGGCTCTTCGACGCTCTCTTACGCTTCATGTGTCCACACCGCTGGCCATCAGGGC 2521  
Qy 845 LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuLys 864  
Db 2522 AAGTCTCTACGTCCAGTGCCAGGGATCCCGCAGGGCTCCATCTCTCCAGCGTCTGCTGC 2581  
Qy 865 SerLeuCystTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu 884  
Db 2582 AGCCTGTGTACGGCGACATGGAGAACAAAGCTCTTTTCGGGGATTCGGCGGAGCGGCTG 2641  
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Db 2642 CTCTCGCTTGGTGGATGATTCTTGTGGTGACACCTCACCTCACCCAGCGCAAAACC 2701  
Qy 905 PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys 924  
Db 2702 TTCTCAGGACCTGGTCCGAGGTGTCCTCGAGTATGGCTGCGTGGTGAACCTTGGCGAAG 2761  
Qy 925 ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet 944  
Db 2762 ACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCAGGGCTTTTGTTCAGATG 2821  
Qy 945 ProAlaHisGlyLeuPheProTyrPyrCysGlyLeuLeuLeuAspThrArgThrLeuGluVal 964  
Db 2822 CCGGCCACCGCCTATTTCCTGGTGGGCGCTGCTGCTGGATACCCGAGCCCTGGAGGTG 2881  
Qy 965 GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg 984  
Db 2882 CAGAGGACCTACTCCAGCTATGCCGAGACCTCCATCAGAGCCAGTCTCACCTTCAACCGC 2941  
Qy 985 GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys 1004  
Db 2942 GGCTTCAAGGCTGGGAGGAACATGCGTGCAGAACTCTTTGGGGTCTTTCGGCTGAAGTGT 3001  
Qy 1005 HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr 1024  
Db 3002 CACAGCCTGTTTCTGGATTTGCAGGTGAACAGGCTCCAGAGCGGTGTCACCAACATCTAC 3061  
Qy 1025 LysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis 1044  
Db 3062 AAGATCTCTCTGCTGAGCGGTACAGGTTTTCAGCATGTGCTGTCAGCTCCCATTTTCAT 3121  
Qy 1045 GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu 1064  
Db 3122 CACCAAGTTTGGGAAGAACCCACATTTTCTCGCGCTCATCTCTGACAGCGGCTCCCTC 3181  
Qy 1065 CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla 1084  
Db 3182 TGCTACTCCATCTCGAAGCCAGAGCGAGGATGTCGCTGGGGCCAGAGGCGCGCC 3241  
Qy 1085 GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeu 1104  
Db 3242 GGCCCTCTGCGCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTG 3301  
Qy 1105 ThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGln 1124  
Db 3302 ACTGACACCGCTGACCTACGTGCGCATCTCTGCGGTCTGCTGAGGAGCCAGACGAG 3361  
Qy 1125 LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsnProAla 1144  
Db 3362 CTGATCGGAAGCTCCCGGGGAGCGCTGACTGCTGCGCTGGAGCGCGCAGCCAGCGCA 3421  
Qy 1145 LeuProSerAspPheLysThrIleLeuAsp 1154  
Db 3422 CTGCGCTCAGACTTCAAGACCATCTCTGGAC 3451

## RESULT 6

US-10-208-243-1  
; Sequence 1, Application US/10208243  
; Publication No. US20030044394A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaeta, Federico C.A.  
; APPLICANT: Geron Corporation  
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune  
; FILE REFERENCE: Response to a Telomerase Antigen  
; CURRENT APPLICATION NUMBER: US/10/208,243  
; CURRENT FILING DATE: 2002-07-30  
; PRIOR APPLICATION NUMBER: US/09/675,321  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/112,006  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898  
; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 4015

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (36)..(3454)

; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)

US-10-208-243-1

Alignment Scores:

Pred. No.: 0 Length: 4015

Score: 6057.00 Matches: 1150

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 99.64% Indels: 0

DB: 14 Gaps: 0

US-08-951-733-20 (1-1154) x US-10-208-243-1 (1-4015)

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DB 2 CAGCGCTGCGTCTGCTGGCAGCGTGGAGCCCTGGCCCGCCGCCGCGATGCGG 61
|||||
QY 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44
|||||
DB 62 CCGCGTCCCGCTGCGCAGCGCGTGGCTCCCTGCTGCGCAGCCACTACCGCGAGTGCTG 121
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QY 45 ProLeuAlaThrPheValArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly 64
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DB 122 CCGCTGGCCACGTTCTGTCGGCGCCTGGGGCCCCAGGGCTGGCGCTGGTGCGAGCGCGG 181
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QY 65 AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla 84
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DB 182 GACCGCGCGCTTTCGCGCGCTGCTGGCCAGTGCCTGGTGGTGGCTGGCGACGCA 241
|||||
QY 85 ArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104
|||||
DB 242 CGCGCGCCCGCGCGCCCTCCCTTCGCCAGGTGTCTGCCTCAAGGAGTGTGGTGGCC 301
|||||
QY 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124
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DB 302 CGAGTGCCTGACAGAGCTGTGCGAGCGCGCGCGAAGAACGTGTGGCTTCGGCTTCGCG 361
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QY 125 LeuLeuAspGlyAlaArgGlyClyProProGluAlaPheThrThrSerValArgSerTyr 144
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DB 362 CTGCTGGACGGGCGCGGGGCCCCCGGAGGCTTCACCCAGCGTGGCGAGCTAC 421
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QY 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuLeuArg 164
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DB 422 CTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGGCTGCGGGCTGCTGCTGGCG 481
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QY 165 ArgValGlyAspAspValLeuValHisLeuAlaArgCysAlaLeuPheValLeuVal 184
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DB 482 CGCGTGGCGACGACGCTGCTGCTACCTGCTGGCAGCTGCGCGCTCTTTGTGCTGGTG 541
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DB 542 GCTCCAGCTCGCCTACCAAGTGTGGGGCGCGCGCTGTACCAAGCTGCGCGTGGCCACT 601
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QY 205 GlnAlaArgProProProHisAlaSerGlyProArgArgLeuGlyCysGluArgAla 224
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QY 225 TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg 244
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1862 GAAGCAGAGGTGAGCAGCATCGGGAAGCCAGGCCGCCCTGCTGACGTCGAGACTCCGC 1921  
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645 PheLeuProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla 664  
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1922 TTTCATCCCAAGCCTGACGGCTGCGCGCGATTGTGAACATGGACTACGTCGTGGGAGCC 1981  
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665 ArgThrPheArgArgGlyLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe 684  
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685 SerValLeuAsnTyrGluArgAlaArgProGlyLeuLeuGlyAlaSerValLeuGly 704  
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725 ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln 744  
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745 AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg 764  
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765 ArgTyrAlaValGlnLysAlaHisGlyHisValArgLysAlaPheLysSerHis 784  
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2342 GTCTCTACCTTGACAGACCTCCAGCGGTATATGCGACAGTTCGTGGCTCACCTGAGGAG 2401  
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825 SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly 844  
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845 LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys 864  
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865 SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu 884  
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2702 TTCCCTCAGACCCCTGTGCTCGAGGTGTCTCTGAGTATGGCTGGGTGAACCTGGGGAAG 2761  
QY  
925 ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet 944  
|||||  
2762 ACAGTGGTGAACCTTCCTGTAGAACGAGGCCCTGGGTGGCAGCGCTTTGTTGATG 2821  
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945 ProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeuGluVal 964  
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2822 CCGGCCACGGCCTATTCCCTGCTGGCGCCTGCTGTGATACCCGACCCCTGGAGGTG 2881  
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965 GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg 984  
|||||  
2882 CAGAGCGACTACTCCAGCTATCCCGGACCTCCATCAGAGCCAGTCTACCTTCAACCGC 2941  
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985 GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys 1004  
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2942 GGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGTCTTGGGCTGAAGTGT 3001  
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1025 LysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis 1044  
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3062 AGATCCTCCTGCTGAGGGGTACAGGTTTACAGCATGTGTGCTGAGCTCCCATTTTCAT 3121  
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1045 GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu 1064  
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3122 CAGCAAGTTTGAAGAACCACATTTTCTGCGGTCTCTCTCAGACGGCTCCCTC 3181  
QY  
1065 CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla 1084  
|||||  
3182 TGTACTCTCCTCTGAAGCCAGAACGAGGATGCTGCTGGGGCCAAAGGCGCGCC 3241  
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1085 GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeu 1104  
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3242 GGCCCTCTGCCCTCCAGGCGGTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3301  
QY  
1105 ThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGln 1124  
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3302 ACTCGACACCGGTCTACCTACGTGCGCACCTCTGGGCTCACTCAGGACGCCACGCGAG 3361  
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1125 LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsnProAla 1144  
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3362 CTGAGTCGGAAGCTCCCGGGAGCGAGCTGACTGCTGCTGAGCGCGCAGCAACCGGCA 3421  
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1145 LeuProSerAspPheLysThrIleLeuAsp 1154  
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3422 CTGCCCTCAGACTTCAAGACCATCTCTGGAC 3451  
Db

## RESULT 7

US-10-054-295-224  
; Sequence 224, Application US/10054295  
; Publication No. US20030044953A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. US20030044953A1el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; Zip: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/054,295  
; FILING DATE: 18-Jan-2002  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/854,050  
; FILING DATE: <unknown>  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-0029300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 224:

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
;

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? NAME/KEY: CDS
? LOCATION: 56..3454
? OTHER INFORMATION: /product= "hTERT"
? /note= "human telomerase reverse
? transcriptase (hTERT) catalytic protein
? component"
?
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US-10-054-295-224

**Alignment Scores:**

Pred. No.:	0	Length:	4015
Score:	6057.00	Matches:	1150
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.64%	Indels:	0
DB:	14	Gaps:	0

US-08-951-733-20 (1-1154) x US-10-054-295-224 (1-4015)

QY	5	GlnArgCysValLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro	24
Db	2	CAGCGCTCGCTCTGCTGCGACGTGGGAAGCCCTGGCCCGCCACCCCGCATGCCG	61
QY	25	ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu	44
Db	62	CGCGTCCCCGCTGCCGAGCGGTGCGTCCCTGCTGCGCAGCCACATACCAGGAGGTGCTG	121
QY	45	ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly	64
Db	122	CCGCTGGCCACGTTCCGTGGCGCGCTGGGCCCCAGGGCTGGCGGTGGTGACAGCGGG	181
QY	65	AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla	84
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QY	85	ArgProProProAlaAlaProSerPheArgGlnValSerCystLeuLysGluLeuValAla	104
Db	242	CGGCGCGCCCCGCGCGCCCTCTCTCCGCCAGGTGCTCTGACGAGGCTGGTGGCC	301
QY	105	ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla	124
Db	302	CGAGTGTGTGACAGAGCTGTGCGAGCGCGCGCAGAACGTGTGGCTTCGGCTTCGGC	361
QY	125	LeuLeuaspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr	144
Db	362	CTGTGTGACGGGGCGCGGGGGCCCCCGGAGGCTTCACCAACAGCGTGGCAGCTAC	421
QY	145	LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuLeuArg	164
Db	422	CTGCCCAACACGGTGACCGACGCNCTCGGGGGAGCGGGGCTGTGTGCTGGCGC	481
QY	165	ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal	184
Db	482	CGCGTGGCGCAGCAGCTGCTGGTTCACTCTCGSCACGCTGCGCGCTCTTGTGTGCTG	541
QY	185	AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr	204
Db	542	GCTCCCAAGTCGCGCTTACCAAGTGTGGGGCGCCGCTGTACCAAGCTCGCGCTGCAC	601

565 LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyr 584  
1682 AAGTTCTCGACGTCGTGATGAGTGTAGTGTGTCGACGCTGCTCAGGTCCTTTCTTTAT 1741  
585 ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer 604  
1742 GTCACGGAGACACAGCTTTCAAAAGAACAGCGCTCTTTTCTACCGGAAGAGTGTCTGGAGC 1801  
605 LysLeuGlnSerIleGlyLeuArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer 624  
1802 AAGTTCAAGCATTTGAATCAGACAGCACTTGAAGAGGGTCAGTGGGAGCTGTCG 1861  
625 GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg 644  
1862 GAAGCAGAGGTACAGCAGCATCGGGAAGCCAGCGCCGCTGCTGACGTCCAGACTCCGC 1921  
645 PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla 664  
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685 SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly 704  
2042 AGCGTCTCAACTACAGCGGGCGCGCGCGCTCTGGCGCCCTCTGTGCTGGGC 2101  
705 LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro 724  
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725 ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrLeuProGln 744  
2162 CGCGCTGACGTACTTGTCAAGGTGGATGTGACGGGCGGTACGACACCATCCCGCCAG 2221  
745 AspArgLeuThrGluValIleAlaSerIleLeuLysProGlnAsnThrTyrCysValArg 764  
2222 GACAGGCTCAGGAGGTATCGCCACCATCATCAAAACCCAGAACACGACTGCTGCGGT 2281  
765 ArgTyrAlaValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis 784  
2282 CGGTATGCGTGTCCAGAAGCGCGCCATGGCAGCTCCGCAAGGCTTCAAGAGCCAC 2341  
785 ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGln 804  
2342 GTCTCTACCTTGACAGACCTCCAGCGGTATATGCGACGTTGCTGCTCACCCTGACGAG 2401  
805 ThrSerProLeuArgAspAlaValValIleGluGlnSerSerLeuAsnGluAlaSer 824  
2402 ACCAGCGCGTGAGGATGCGGTGTCATCGACGACAGCTCTCCCTGATGAGGCCAGC 2461  
825 SerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIleArgGly 844  
2462 AGTGGCCTCTTCGACGCTCTCTACGCTTATGTGCCACACCGCGTGCATCAGGGGC 2521  
845 LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys 864  
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865 SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu 884  
2582 AGCGTGTCTACGGCAGCATGAGAAACAGCTGTTTGGGGGATTCGGCGGAGCGGCTG 2641  
885 LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr 904  
2642 CTCCTCGGTTTGGTGGATGTTCTGTTGGTGACACCTCACCTCACCCAGCGGAACC 2701  
905 PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys 924  
2702 TTCCTCAGGACCGTGTGCGAGGTGCTGAGTATGCTGCTGCTGCTGCTGCTGCTGCTG 2761  
925 ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet 944

2762 ACAGTGGTGAACCTTCCTGTAGAAGACGAGGCCCTGGGTGGACGGCTTTGTTTCAGATG 2821  
945 ProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeuGluVal 964  
2822 CCGGCCACGGCCATTTCCTCGTGGCGCTGCTGCTGATACCCGGACCTGGAGGTG 2881  
965 GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg 984  
2882 CAGAGGACTATCCAGCTATGCCGAGACTTCATCAGAGCCAGTCTCAGCTTCAACCGC 2941  
985 GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys 1004  
2942 GCGTTCAAGGCTGGAGGAACATGCGTCGCAACTCTTTGGGCTCTTGGGCTGAAGTGT 3001  
1005 HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr 1024  
3002 CACAGCTGTCTTGGATTGCAAGTGAACAGCTCCAGACGGTGTGCACCAACATCTAC 3061  
1025 LysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis 1044  
3062 AGATCCTCTGCTGAGCGGTACAGGTTTCACGATGTGTGCTGAGCTCCCATTTTCAT 3121  
1045 GlnGlnValTrpLysAsnProThrPheLeuArgValIleSerAspThrAlaSerLeu 1064  
3122 CAGCAAGTTTGGAGAACCACCATTTTCTCGCGTCACTCTGNACAGGCTCCCTC 3181  
1065 CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla 1084  
3182 TGCTACTCATCTGAAAGCAAGACGACGAGGTGCTGCTGGGCGCAAGGGCGCGCC 3241  
1085 GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLysLeu 1104  
3242 GCGCCCTCTGCCCTCCAGGCGGTGACGTGGCTGCTGCGCCACCAAGCATTCCTGCTCAAGCTG 3301  
1105 ThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGln 1124  
3302 ACTCGACCGCTGACCTACGTGCCACTCTCTGGGCTCACTCAGGACGCGCCAGCGAG 3361  
1125 LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsnProAla 1144  
3362 CTGAGTCGGAAGCTCCCGGGAGCGCTGACTGCTGAGCGCGCGCAGCAACCCGGCA 3421  
1145 LeuProSerAspPheLysThrIleLeuAsp 1154  
3422 CTGCCCTCAGACTTCAAGACCATCTCTGGAC 3451

## RESULT 8

US-10-054-611-224  
; Sequence 224, Application US/10054611  
; Publication No. US20030059787A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. US20030059787A1el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:			
APPLICATION NUMBER:	US/10/054,611		
FILING DATE:	18-Jan-2002		
CLASSIFICATION:	536		
PRIOR APPLICATION DATA:			
APPLICATION NUMBER:	08/854,050		
FILING DATE:	<Unknown>		
APPLICATION NUMBER:	US 08/846,017		
FILING DATE:	25-APR-1997		
APPLICATION NUMBER:	US 08/844,419		
FILING DATE:	18-APR-1997		
APPLICATION NUMBER:	US 08/724,643		
FILING DATE:	01-OCT-1996		
ATTORNEY/AGENT INFORMATION:			
NAME:	Apple, Randolph T.		
REGISTRATION NUMBER:	36,429		
REFERENCE/DOCKET NUMBER:	015389-00293005		
TELECOMMUNICATION INFORMATION:			
TELEPHONE:	(415) 576-0200		
TELEFAX:	(415) 576-0300		
INFORMATION FOR SEQ ID NO: 224:			
SEQUENCE CHARACTERISTICS:			
LENGTH:	4015 base pairs		
TYPE:	nucleic acid		
STRANDEDNESS:	single		
TOPOLOGY:	linear		
MOLECULE TYPE:	cdna		
FEATURE:			
NAME/KEY:	CDS		
LOCATION:	56..3454		
OTHER INFORMATION:	/product= "htrp"		
/note=	"human telomerase reverse		
transcriptase (htrp) catalytic protein	component"		
SEQUENCE DESCRIPTION: SEQ ID NO: 224:			
US-10-054-611-224			
Alignment Scores:			
Pred. No.:	0		
Score:	6057.00		
Percent Similarity:	100.00%		
Best Local Similarity:	100.00%		
Query Match:	99.64%		
DB:	14		
US-08-951-733-20 (1-1154) x US-10-054-611-224 (1-4015)			
QY	5	GlnArgCysValLeuLeuArgThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro	24
Db	2	CAGCGCTGGCTCCTCTCGGCACGTGGGAAGCCCTGGCCCGCCACCCCGCGATGCCG	61
QY	25	ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu	44
Db	62	CGCGTCCCGCTGCGAGACGTCGGCTCCCTGCTGCGCAGGCACCTACCCGAGGTGCTG	121
QY	45	ProLeuAlaThrPheValArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly	64
Db	122	CGCGTGGCCACGTTCTGTCGGCGCTGGGGCCCCAGGGCTGGGTGGTGGTGGTGGTGG	181
QY	65	AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla	84
Db	182	GACCCGGCGGCTTCCCGCGCTGGTGGCCAGTGCCTGGTGGTGGTGGTGGTGGTGG	241
QY	85	ArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla	104
Db	242	CGCGCGCCCGCGCGCCCGCTCTTCGCGAGGTGCTTCCTCGCGAGGAGCTGGTGGCC	301
QY	105	ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla	124
Db	302	CGAGTGTCTCAGAGGCTGTGCGAGCGCGGCGAAGACGTGCTGGCTTCGGCTTCGGC	361
QY	125	LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr	144

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QY 505 AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys 524
DB 1502 AACGAACGCCGCTTCTCAGSAACACCAAGAAGTTTCATCTCCCTGGGGAAGCATGCGCAAG 1561
QY 525 LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg 544
DB 1562 CTTCTCGCTGCAGGAGCTGACGTGGGAAGATGACGCTGGCGGACTGCGCTTGGCTGCCACG 1621
QY 545 SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluLeuAla 564
DB 1622 AGCCAGGGGTTGGCTGTCTTCGGCGCCGAGACACCGCTCGTGGAGAGATCCCTGGCC 1681
QY 565 LysPheLeuHisTrpLeuMetSerValTyValValGluLeuLeuArgSerPhePheTy 584
DB 1682 AAGTTCTCATCTGGCTGATGAGTGTGTACGTGCGAGCTGCTCAGGTCTTCTTTTAT 1741
QY 585 ValThrGluThrPheGlnLysAsnArgLeuPhePheTyArgLysSerValTrpSer 604
DB 1742 GTCACGGACACCGTTTCAAGAAGACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGC 1801
QY 605 LysLeuGlnSerIleGlyLysGlnHisLeuLysArgValGlnLeuArgGluLeuSer 624
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QY 625 GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg 644
DB 1862 GAAGCAGAGGTGAGGCAGCATCGGAAGCAGCGCGCGCTGCTGACGTCCAGACTCCGC 1921
QY 645 PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyValValGlyAla 664
DB 1922 TTCATCCCCAAGCTGACGGGCTGGCGCGATGTGTGAACATGACATGCTCGTGGAGCC 1981
QY 665 ArgThrPheArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe 684
DB 1982 AGAAGCTTCCGCAGAGAAAAGAGGCGGAGCGTCTCACCTCGAGGGTGAAGCACTGTTC 2041
QY 685 SerValLeuAsnTyGluAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly 704
DB 2042 AGCGTGCTCAACTACAGCGGGCGGCGCGCCCGCGCTCTGGCGGCTCTGTGTGGGC 2101
QY 705 LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro 724
DB 2102 CTGGAGATATCCACAGGCGCTGGCGACCTTCGTGCTCGTGGCGGCCAGGACCG 2161
QY 725 ProProGluLeuTyPheValLysValAspValThrGlyAlaTyArgThrIleProGln 744
DB 2162 CGGCTGAGCTGACTTTGTCAAGGTGGATGTACGGGCGGTACGACACCATCCCCAG 2221
QY 745 AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrcysValArg 764
DB 2222 GACAGGCTCAGGAGGTATCGCCAGCATCAAAACCCAGAACACGTACTGCGTGGCT 2281
QY 765 ArgTyAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis 784
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QY 785 ValSerThrLeuThrAspLeuGlnProTyMetArgGlnPheValAlaHisLeuGlnGlu 804
DB 2342 GTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTGCTGGCTCACCTGCAAGG 2401
QY 805 ThrSerProLeuArgAspAlaValValIleGluGlnSerSerLeuAsnGluAlaSer 824
DB 2402 ACCAGCCGCTGAGGAGTCCGTCGTCATCGAGCAGAGCTCTCCCTGAATGAGGCGACG 2461
QY 825 SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly 844
DB 2462 AGTGGCTCTTCGACGCTCTCTACGCTTCATGTGCCACACCGCCGTCGCGATCAGGGGC 2521
QY 845 LysSerTyValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys 864
DB 2522 AAGTCTACGTCCAGTGCCAGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTGC 2581
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QY 865 SerLeuCysTyrcGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu 884
DB 2582 AGCCTGTGTACGGGCACATGGAGAACAAAGCTGTTTTCGGGGATTTCGGGGAGGCGTG 2641
QY 885 LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr 904
DB 2642 CTTCTCGCTTGGTGGATGATTTCTTTGTTGGTGACACCTCACCTCACCGCAAAACC 2701
QY 905 PheLeuArgThrLeuValArgGlyValProGluTyrcGlyCysValValAsnLeuArgLys 924
DB 2702 TTCCTCAGGACCTGTGTCGAGGTGCTCGTAGTATGGCTGCTGTAACCTTGCGGAAG 2761
QY 925 ThrValValAsnPheProValGluAspGluAlaLeuGlyClyThrAlaPheValGlnMet 944
DB 2762 ACAGTGGTGAACCTTCCTGTAGAAGACGAGGCGCTGGGTGGCAGCGCTTTGTTCAGATG 2821
QY 945 ProAlaHisGlyLeuPheProTyrcGlyLeuLeuLeuAspThrArgThrLeuGluVal 964
DB 2822 CCGGCCACGCGCTATTCCCTGGTCGGCCTGCTGCTGGATACCGGACCTTGAGGTCG 2881
QY 965 GlnSerAspTyrcSerSerTyrcAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg 984
DB 2882 CAGAGCGACTACTCCAGCTATGCCGCGAGCTCCATCAGAGCCAGTCTCACCTTCAACCGC 2941
QY 985 GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCys 1004
DB 2942 GGTCTCAAGGCTGGGAGAACATGCTGCGCAAACTCTTTGGGCTCTTGGGCTGAAGTGT 3001
QY 1005 HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTy 1024
DB 3002 CACAGCTGTTCGTGGATTTGCAGGTGAACAGCTCCAGCGGTGCACCAACATCTAC 3061
QY 1025 LysIleLeuLeuLeuGlnAlaTyrcPheHisAlaCysValLeuGlnLeuProPheHis 1044
DB 3062 AAGATCTCTCTGCTGAGGCGTACAGGTTTCACGCATGTGTGTCAGCTCCCATTTTCAT 3121
QY 1045 GlnGlnValTrpLysAsnProThrPheLeuArgValIleSerAspThrAlaSerLeu 1064
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QY 1145 LeuProSerAspPheLysThrIleLeuAsp 1154
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## RESULT 9

US-10-105-963-1

; Sequence 1, Application US/10105963

; Publication No. US20030068818A1

; GENERAL INFORMATION:

; APPLICANT: Geron Corporation

; APPLICANT: Denning, Chris

; APPLICANT: Clark, A. John

; APPLICANT: Schiiff, J. Michael

; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human

; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection Syst

; TITLE OF INVENTION: Recombination

; FILE REFERENCE: 731/002



; CURRENT APPLICATION NUMBER: US/10/105,963  
; CURRENT FILING DATE: 2002-03-21  
; PRIOR APPLICATION NUMBER: US 60/277,811  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 4015  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (56)..(3454)  
; OTHER INFORMATION:  
US-10-105-963-1

Alignment Scores:  
Pred. No.: 0 Length: 4015  
Score: 6057.00 Matches: 1150  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.64% Indels: 0  
DB: 14 Gaps: 0

US-08-951-733-20 (1-1154) x US-10-105-963-1 (1-4015)

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Qy	25	ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu	44
Db	62	CGCGCTCCCGCTGCCGAGCGCTGCGTCCCTGCTGCGACGCCACTACCGCGAGGTGCTG	121
Qy	45	ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly	64
Db	122	CCGCTGGCCAGCTTCGTGCGGCGCTGGGGCCCGAGGCTGGCGCTGGTGCGACGCGGG	181
Qy	65	AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla	84
Db	182	GACCGCGCGGCTTTCCGCGCGCTGGTGGCCAGTGCCTGGTGTGCTGCGTGGGACGCA	241
Qy	85	ArgProProAlaAlaProSerPheArgGlnValSerCysLeuValCysValProTrpAspAla	104
Db	242	CGGCGCGCGCGCGCGCGCGCTCCCTCCGCGAGGTGCTGCTGCTGAAGGAGCTGGTGGCC	301
Qy	105	ArgValLeuGlnArgLeuCysGluArgGlyValAlaLysAsnValLeuAlaPheGlyPheAla	124
Db	302	CGAGTGTGCAGAGGCTGTGGAGCGCGCGCGCGAGACGTGCTGGGCTTCGCGTTCGCG	361
Qy	125	LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr	144
Db	362	CTGCTGGACGGGCGCGCGGCGCGCGCGCGCGCGCGCTTACCACACGCTGCGCAGCTAC	421
Qy	145	LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuLeuArg	164
Db	422	CTGCCAACACGCTGACCGACGCTGCGGGGAGCGGGGCGTGGGGGCTGCTGCTGCGC	481
Qy	165	ArgValGlyAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal	184
Db	482	CGCGTGGCGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	541
Qy	185	AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr	204
Db	542	GCTCCAGCTGCGCTACCGAGTGTGGGCGCGCGCGCTGTACCAGCTTCGCGCTGCCACT	601
Qy	205	GlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGluArgAla	224
Db	602	CAGCGCGCGCGCGCGCGCGCTAGTGGACCGCGAGGCGCTCTGGGATCGCAACGCGGC	661
Qy	225	TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg	244
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Qy	245	ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla	264
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Db	1502	AACGACGCGCTTCTCTCAGGACACCAAGAGTTCATCTCCCTGGGAGACATGCCAAG	1561
Qy	525	LeuSerLeuGlnLeuLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg	544
Db	1562	CTCTCGCTGAGGAGCTGAGCTGGAGATGAGCTGGGGGACTGCGCTTGGCTGCGCAGG	1621
Qy	545	SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIleLeuAla	564
Db	1622	AGCCAGGGGTGGCTGTCTGTCGCGCGCAGAGCAGCGCTGTGCTGTGAGGAGATCCTG	1681
Qy	565	LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyr	584
Db	1682	AACTTCTGCACTGGCTGATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1741
Qy	585	ValThrGlnThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer	604
Db	1742	GTCACGAGGACACGCTTCAAAAGACAGGCTCTTTTCTACCGGAGAGGTGTCTGAGC	1801



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QY 605 LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer 624
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Db 1862 GAAGCAGAGGTTCAGGCAGCATCGGAAGCAGCGCCGCCCTGCTGACGTCCAGACTCCGC 1921
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QY 685 SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly 704
Db 2042 AGCGTGCTCAACTACGAGCGGCGCGGCCCGCCCTCTGCGGCCCTCTGTGTGGGC 2101
QY 705 LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro 724
Db 2102 CTGGAGCATATCCAGAGGCGCTTGGCGACCTTCTGCTGCTGCTGCGGCGCCAGGACCGC 2161
QY 725 ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln 744
Db 2162 CGCCCTGACTACTTGTCAAGGTGGATGTGACGGGCGGTACGACACCATCCCGCCAG 2221
QY 745 AspArgLeuThrGluValIleAlaSerIleLysProGlnAsnThrTyrCysValArg 764
Db 2222 GACAGGCTCAGGAGGTATCCGCCAGCATCATCAAAACCCAGAACACGTACTGCGTGC 2281
QY 765 ArgTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis 784
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Db 2342 GTCTCTACCTGCACAGACCTCCAGCGGTACATGCACAGTTCGTGCTCACCCTGGAG 2401
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Db 2462 AGTGGCCCTTCGACGCTCTCTTACGCTTCATGTGCCACACGCGGTGCGCATCAGGGC 2521
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Db 2522 AAGTCTACGTCCAGTCCAGGGGATCCGCGAGGGCTCCATCCTCTCCACGCTGCTCTGC 2581
QY 865 SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu 884
Db 2582 AGCCTGTGCTACGCGACATGAGAACACAGCTGTTGCGGGATTCGCGGGACGGGCTG 2641
QY 885 LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr 904
Db 2642 CTCCCTGCGTGTGGTGATGATTTCTTGTGTGTGACACCTCACCTCACCCACGCAAAACC 2701
QY 905 PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys 924
Db 2702 TTCCCTCAGACCCCTGTCGAGGTGCTCGTAGTATGGCTGGCTGGAACCTGGCGAAG 2761
QY 925 ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet 944
Db 2762 ACAGTGGTGAACTTCCCTGTAGAACAGGCGCCCTGGGTGGCACCGCTTTGTTTCAGATG 2821
QY 945 ProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeuGluVal 964
Db 2822 CGGGCCACGGCGCTATCCCTGTGTGCGCGCTGCTGCTGGATACCCGACCCCTGGAGGTG 2881
QY 965 GlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg 984

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3002 CACAGCGCTTTCTTGATTTGCAGGTGAACAGCGCTCCAGACGGTGTGCACCAACATCTAC 3061
1025 LysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis 1044
3062 AGATCTCTCTGCTGCGAGCGGTACAGGTTTACGATGTGTGCTGCGCTCCCATTTTCAT 3121
1045 GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu 1064
3122 CAGCAAGTTTGAAGAAGCCACATTTTCTCGCGGTCTATCTCTGACAGGCGCTCCCTC 3181
1065 CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla 1084
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RESULT 10
US-10-044-692-1
; Sequence 1, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
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, APPLICATION NUMBER: US 08/854,050
, FILING DATE: 09-MAY-1997
, APPLICATION NUMBER: US 08/851,843
, FILING DATE: 06-MAY-1997
, APPLICATION NUMBER: US 08/846,017
, FILING DATE: 25-APR-1997
, APPLICATION NUMBER: US 08/844,419
, FILING DATE: 18-APR-1997
, APPLICATION NUMBER: US 08/724,643
, FILING DATE: 01-OCT-1996
, ATTORNEY/AGENT INFORMATION:
, NAME: Apple, Randolph T.
, REGISTRATION NUMBER: 36,429
, REFERENCE/DOCKET NUMBER: 015389-0026000US
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (415) 576-0200
, TELEFAX: (415) 576-0300
, INFORMATION FOR SEQ ID NO: 1:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 4015 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: cDNA
, FEATURE:
, NAME/KEY: CDS
, LOCATION: 56..3454
, OTHER INFORMATION: /product= "hTfT"
, /note= "human telomerase reverse
, transcriptase (hTfT) catalytic protein
, component"
, SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-692-1

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Alignment Scores:	
Pred. No.:	0
Score:	6057.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	99.64%
DB:	14
Alignments:	14
Matches:	4015
Mismatches:	0
Indels:	0
Gaps:	0

US-08-951-733-20 (1-1154) x US-10-044-692-1 (1-4015)

QY	5	GlnArgCysValLeuLeuAThrTrpGluAlaLeuAlaProAlaThrProAlaMetPro	24
Db	2	CAGCGCTCGCTGCTGCACACGTGGGAAGCCCTGGCCCGGCACCCCGCATGCCG	61
QY	25	ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu	44
Db	62	CGCGTCCCGCTGCCAGCGTCGCTCCCTGCTGCAGCCACCTACCGCGAGTGCTG	121
QY	45	ProLeuAlaThrPheValArgLeuGlyProGlnGlyTrpArgLeuValGlnArgGly	64
Db	122	CCGCTGGCCACGTCGTGCGCGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCCGG	181
QY	65	AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrpAspAla	84
Db	182	GNACCGGGGGTTCCTCCGGCGCGCTGGTGCCACGTGCCTGCTGCGTGGCCACGCA	241
QY	85	ArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla	104
Db	242	CGGCGCGCCCCCGCGGCCCTCCTTCGCGAGGTGCTGCTGAAGAGCTGGTGGCC	301
QY	105	ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla	124
Db	302	CGAGTGTGCAGAGGTGTGGCAGCGGGCGGAGAACGTGCTGGCTTCGGCTTCGGCG	361
QY	125	LeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArgSerTyr	144
Db	362	CTGTGGACGGGGCCCGGGGGCCCCCGAGGCCCTTCACACACAGCGTGGCGACCTAC	421
QY	145	LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuLeuArg	164

Db	422	 CTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCTGGGGGCTGCTGCTGGCG	481
Qy	165	ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal	184
Db	482	CGCGTGGCGACGACGCTGCTGGTTACCTGCTGGCACGCTGCGCGCTCTTTGTGGTGGT	541
Qy	185	AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr	204
Db	542	GCTCCAGCTGCGCCTACCAAGTGTGCGGGCGCGCTGTACCAAGCTCGGGCGTGCCT	601
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Qy	225	TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg	244
Db	662	TGGAACCATACGCTCAGGAGCGCGGGTCCCTTGGGCTGTCCAGACCCCGGGTCCGAGG	721
Qy	245	ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla	264
Db	722	AGGCGGGGGCAGTGCAGCCGAAGTCTGCGTGTGCCAAGAGGCCAGGCGTGGCGCT	781
Qy	265	AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr	284
Db	782	GCCCTTGAGCGGAGCGACGCCGCTGGGCGAGGGTCTCTGGGCGCCACCGGGCAGGACG	841
Qy	285	ArgGlyProSerAspArgGlyPheCysValValSerProAlaAlaArgProAlaGluAla	304
Db	842	CGTGGACCGAGTGACCGTGGTTCGTGTGGTGTCACCTGCCACACCGCGCAAGAGCC	901
Qy	305	ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln	324
Db	902	ACCTTTTGGAGGTGGCTCTCTGGCACGGCGCCACTCCCACCATCTCGTGGGCGCCGAG	961
Qy	325	HisHisAlaGlyProProSerThrSerArgProProArgProTrpArgProCysPro	344
Db	962	CACCACGCGGCGCCCATCCATCGCGGCGCACAGCTCCTGGGACACGCTTGTCCC	1021
Qy	345	ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg	364
Db	1022	CCGGTGTACGCGGAGCAAGCACTCCTTACTTCTCAGCGCAACAAGGACAGCTGCGG	1081
Qy	365	ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu	384
Db	1082	CCCTCCTTCTACTCAGCTCTCTGAGGCCACGCTGACTGGCGCTGGGAGGCTCGTGGAG	1141
Qy	385	ThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuProArgLeu	404
Db	1142	ACCATCTTCTGGTTCAGGCGCTGGATGCCAGGGACTCCCCGACAGTTGCCCGCGCTG	1201
Qy	405	ProGlnArgTyrTrpGlnMetArgProPheLeuGluLeuLeuGlyAsnHisAlaGln	424
Db	1202	CCCCAGCGCTACTGGCAAAATGCGGCCCTGTTCCTGGAGCTGCTTGGGAACACAGCGCAG	1261
Qy	425	CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla	444
Db	1262	TGCCCTACGGGTGCTCCTCAAGACGCACTGCCCGTGGCGAGTGGGTCAACCCACGCA	1321
Qy	445	AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluAsp	464
Db	1322	GCGCGTCTGTGCCGGGAGAGCCGCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGAC	1381
Qy	465	ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGlnValTyr	484
Db	1382	ACAGACCCCGTGGCTTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCTGGCAGGTGTAC	1441
Qy	485	GlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySerArgHis	504
Db	1442	GGCTGTGTGGGCGCTGCCCTGGCGCGGCTGGTGGCCCGAGGCTCTGGGGCTCCAGGCAC	1501
Qy	505	AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys	524

Db	1502	AACGAACGGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGAGCATGCCAAG	1561
QY	525	LeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg	544
Db	1562	CTCTCGCTGCAGGAGTGAGTGGAAAGATGAGCGTGCAGGACTGCGCTTGGCTGCAGG	1621
QY	545	SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLeuAla	564
Db	1622	AGCCCAAGGGTTGGCTGTCTCGCGCCGAGACACCGTCTGGCTGAGGAGATCCTGGCC	1681
QY	565	LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyr	584
Db	1682	AACTTCTCGACTGGCTGATGAGTGAGTGTAGCTGCTGAGTCTTCTTTTAT	1741
QY	585	ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer	604
Db	1742	GTCAAGGAGACCAAGTTCAAAAGAACAAGCTCTTTTCTACCGAAGAGTGTCTGGAGC	1801
QY	605	LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer	624
Db	1802	AACTTCAAGCAATTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGAGCTGTGC	1861
QY	625	GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg	644
Db	1862	GAAGCAGAGGTCAAGCAGCATCGGAAGCAGCGCCGCTGCTGAGCTCCAGACTCCGC	1921
QY	645	PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla	664
Db	1922	TTTATCCCCAAGCTGACGGCTGCGCGCGATTTGTGAACATGACTACCTGCTGGGAGCC	1981
QY	665	ArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe	684
Db	1982	AGAACGTTCGCGAGAAAGAGGGCGGAGCGTCTCACTTCGAGGGTGAAGGCACGTGTC	2041
QY	685	SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly	704
Db	2042	AGCGTGTCAACTACGAGCGGGCGGCGCGCCGCTCTCGGGCGCTCTGTGCTGGC	2101
QY	705	LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro	724
Db	2102	CTGGAGCATATCCAGAGCGCTGGCGCACCTTCGCTGCTGCGGGCCAGGACCCG	2161
QY	725	ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln	744
Db	2162	CCGCTTACGCTGACCTTTGTCAGGTGGATGTGACGGCGCGTACACACCATCCCCCAG	2221
QY	745	AspArgLeuThrGluValIleAlaSerIleLysProGlnAsnThrTyrCysValArg	764
Db	2222	GACAGGCTCAGGAGGTCTCGCCAGCATCATCAAAACCCAGAACACGTACTCGTGGCT	2281
QY	765	ArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis	784
Db	2282	CGGTATGCGGTGTCAGAGGCGGCCCATGGCGACGTGCGCAAGGCCTTCAAGAGCCAC	2341
QY	785	ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu	804
Db	2342	GTCTCTACCTTGCACACCTTCCAGCGGTACATCGGACGTCTGGCTCACCCTGCAGGAG	2401
QY	805	ThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGluAlaSer	824
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QY	825	SerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIleArgGly	844
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Db	2582	AGCTGTGTACGGCCACATGGAGAACAGCTGTTTGGCGGGGATTCGGGGGAGGGCTG	2641
QY	885	LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr	904
Db	2642	CTCTCGTGTGTGTGATGATTCTTGTGTGTGACACCTCACCTCACCGCGAAAC	2701
QY	905	PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys	924
Db	2702	TTCTCTCAGGACCTGTGTGAGGTGTCCCTGTAGTGTGCTGTGCTGTGTAACCTTGC	2761
QY	925	ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet	944
Db	2762	ACAGTGTGAACCTTCCCTGTAGAGAGAGAGCCCTGGGTGGCAGCGCTTTGTTCAGATG	2821
QY	945	ProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeuGluVal	964
Db	2822	CCGGCCACCGGCTATTTCCCTGTGTGCGGCTCTGCTGTGATACCGGACCTTGGAGTG	2881
QY	965	GlnSerAspTyrSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArg	984
Db	2882	CAGAGGACTACTCCAGCTATGCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGC	2941
QY	985	GlyPheLysAlaGlyArgAsnMetArgLysLeuPheGlyValLeuArgLeuLysCys	1004
Db	2942	GGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTCTTTGGGTCTTGGCGCTGAAGTG	3001
QY	1005	HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr	1024
Db	3002	CACAGCTGTCTTGTGATTTGCAGGTGAACAGCTCCAGACGGTGTGCACCAACATCTAC	3061
QY	1025	LysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis	1044
Db	3062	AGATCTCTCTGCTGACGGGTACAGTTTACAGCATGTGTGCTGAGCTCCCATTTTCAT	3121
QY	1045	GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu	1064
Db	3122	CAGCAAGTTTGGAGAACCACACATTTTCTCGCGTCTATCTTGACAGCGCTCCCTC	3181
QY	1065	CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla	1084
Db	3182	TGCTACTCTCATCTGAAAGCAAGACGACGGATGTCTGCTGGGGCCAAAGGGCGCGCC	3241
QY	1085	GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeu	1104
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QY	1125	LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsnProAla	1144
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## RESULT 11

US-10-044-539-1

; Sequence 1, Application US/10044539

; Publication No. US2003010093A1

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND

; THERAPEUTIC METHODS

; NUMBER OF SEQUENCES: 335

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,539

FILING DATE: 11-Jan-2002

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-0026000US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4015 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 56..3454

OTHER INFORMATION: /product= "hprt"

/note= "human telomerase reverse

transcriptase (hprt) catalytic protein

component"

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-044-539-1

Alignment Scores:

Pred. No.: 0 Length: 4015

Score: 6057.00 Matches: 1150

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 99.64% Indels: 0

DB: 14 Gaps: 0

US-08-951-733-20 (1-1154) x US-10-044-539-1 (1-4015)

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Db 2 CAGCGCTGGCTGCTGGCAGCTGGGAGCCCTGGCCCGGCCACCCCGCGCATGCCG 61

Qy 25 ArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGluValLeu 44

Db 62 CGCGCTCCCGCTCCGAGCGCTGCGCTCCCTGTGCGCAGCCACTACCGGAGTGCTG 121

Qy 45 ProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGlnArgGly 64

Db 122 CCGGTGCCACGTTCTGGCGCGCTGGGGCCCCCAGGGCTGGGCTGGTGACGGCGGG 181

Qy 65 AspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyrPaspAla 84  
Db 182 GACCCGGCGGCTTCCCGCGCGCTGGTGCCAGTCGCTGGTGCTGGCTGGACGCA 241  
Qy 85 ArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAla 104  
Db 242 CGGCGCGCCCGCGCGCGCTTCCCTCCGCGCAGGTGCTCTGCTCAAGGAGCTGGTGCC 301  
Qy 105 ArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAla 124  
Db 302 CGAGTGCTGCAGAGGCTGTGCGAGCGCGCGGCGAAGACGCTGCTGGCTTCGGCTCCG 361  
Qy 125 LeuLeuAspGlyAlaArgGlyGlyProGlnAlaPheThrThrSerValArgSerTyr 144  
Db 362 CTGCTGGACGGGCG 421  
Qy 145 LeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeuArg 164  
Db 422 CTGCCAACACGCTGACCGACGCTGCGGGGAGCGGGGCTGGGGCTGCTGCTGGCGC 481  
Qy 165 ArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuVal 184  
Db 482 CGCGTGGCGCAGCGCTGCTGCTTCACTGCTGCGCACGCTGCGCGCTCTTTGCTGGTG 541  
Qy 185 AlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThr 204  
Db 542 GCTCCAGCTGGCGCTACCGAGTGTGCGGGCGCGCGCTGTACCGCTGCGGCTGCCACT 601  
Qy 205 GlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGluArgAla 224  
Db 602 CAGCGCGCGCGCGCGCGCGCTAGTGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 661  
Qy 225 TrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGlyAlaArg 244  
Db 662 TGGAAACCATAGCGTCAGGGAGCGCGGGTCCCGCTGGCGCTGCCACCGCGCGGTCGAGG 721  
Qy 245 ArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArgGlyAla 264  
Db 722 AGCGCGGGGCGAGTGGCGCGCGAGTCTGCGTGGCCAGAGCGCGCGCGCGCGCGCGCT 781  
Qy 265 AlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGlyArgThr 284  
Db 782 GCCCTGAGCGCGAGCGCGCGCGCTGGCGAGGGTCTCTGGCGCGCGCGCGCGCGCGCG 841  
Qy 285 ArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGluAla 304  
Db 842 CGTGACCGAGTGACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 901  
Qy 305 ThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGln 324  
Db 902 ACCTCTTTGGAGGGTGGCTCTCTGGCACGGCGCGCGCGCGCGCGCGCGCGCGCGCG 961  
Qy 325 HisHisAlaGlyProProSerThrSerArgProProArgProTyrPaspThrProCysPro 344  
Db 962 CACCACGGCG 1021  
Qy 345 ProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGlnLeuArg 364  
Db 1022 CCGGTGTACCGCGAGACCAAGCACTCTCTACTCTCTCAGGCGCAGCAAGGAGCAGCTGGG 1081  
Qy 365 ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu 384  
Db 1082 CCCTCTTCTCTACTCAGCTCTCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1141  
Qy 385 ThrLePheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuProArgLeu 404  
Db 1142 ACCATCTTCTGGGTTCCAGGCGCTGGATGCCAGGGACTCCCGCAGGTTGCCCGCGCTG 1201  
Qy 405 ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHisIslaGln 424  
Db 1202 CCCCAGCGCTACTGGCAAACTGGGCGCGCTGTCTTCTGTGGAGTGTCTTGGGAACACCGCG 1261

Qy	425	CysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThrProAla	444	Db	2342	GTCTCTACCTTGCAGACCTCCAGCCGTCATACGACAGTTCGTGCTACCTCTCAGGAG	2400
Db	1262	TGCCCTTACCGGGTGTCTTCTCAAGACCACTGCCGCTGCGAGTGGGTCAACCCAGCA	1321	Qy	805	ThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGluAlaSer	824
Qy	445	AlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGluGluAsp	464	Db	2402	ACACGCCGCTGAGGATGCCGTGTCATCGACAGAGCTCTCTCTGATGATGAGCGACG	2461
Db	1322	GCCGGTGTCTGTGCCGGGAGAGCCCGAGGGCTCTGTGGCGGCCCGGAGGAGGAC	1381	Qy	825	SerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGly	844
Qy	465	ThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGlnValTyr	484	Db	2462	AGTGGCTCTTCCAGCGTCTTCTTCCATACGTCACACCGCTGCGCATCAGGGCG	2521
Db	1382	ACAGACCCGCTGCGCTGGTGACCTGCTCCGCCAGCACAGACCCCTGGCAGGTGTAC	1441	Qy	845	LysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCys	864
Qy	485	GlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySerArgHis	504	Db	2522	AAGTCTCTACCTGACGTGCCAGGGGATCCCGACGGCTCCATCTCTCCACGCTGCTGC	2581
Db	1442	GGCTTCGTGGGGCTGCCCTGCGCGGCTGGTGCCTCCCGACGGCTCTGGGGCTCCAGGCAC	1501	Qy	865	SerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeu	884
Qy	505	AsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLys	524	Db	2582	AGCTGTGCTACCGCGACATGGAGAACAGCTGTTTGGGGGATCTGGCGGGAGGGCTG	2641
Db	1502	AACGAACCGCGCTTCTTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAG	1561	Qy	885	LeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThr	904
Qy	525	LeuSerLeuGlnLeuLeuThrTrpLysMetSerValArgAspCysAlaTrpLeuArgArg	544	Db	2642	CTCTCGGTTTGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCACGCGAAAAACC	2701
Db	1562	CTCTCGCTGACGAGCTGACGTGAAGATGACGTGCGGACTCCGCTTGGCTGCGCAGG	1621	Qy	905	PheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLys	924
Qy	545	SerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLeuAla	564	Db	2702	TTCTCTCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTTCCGGAAG	2761
Db	1622	AGCCAGGGGTGGCTGTGTTCCGGCGCAGACACCGCTGCGGTGAGGAGATCTGGCC	1681	Qy	925	ThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMet	944
Qy	565	LysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPheTyr	584	Db	2762	ACAGTGGTGAACTTCCCTGTAGAAAGACGAGGCCCTGGGTGGCAGGGCTTTGTTCAGATG	2821
Db	1682	AAGTTCCTGACCTGGCTGATGAGTGTGTAGCTGTGAGCTGTCTCAGGTCTTCTTTTAT	1741	Qy	945	ProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeuGluVal	964
Qy	585	ValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrpSer	604	Db	2822	CCGGCCACGGCTATTCCCTGGTGGCGCTGCTGCTGGATACCCGAGACCTGGAGGTG	2881
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Qy	605	LysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSer	624	Db	2882	CAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGC	2941
Db	1802	AAGTTGCAAGCACTTGAATCAGACAGCACTTGAAGAGGTGCGAGCTGCGGGAGCTGCG	1861	Qy	985	GlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuLeuArgLysCys	1004
Qy	625	GluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArg	644	Db	2942	GGCTTCAGGCTGGGAGAACATCGCTGCACAACTCTTTGGGGTCTTTCGGCTGAGTGT	3001
Db	1862	GAAGCAGAGGTACGAGACATCGGGAAGCAGGCCCGCCCTGCTGAGCTCCAGACTCCGC	1921	Qy	1005	HisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyr	1024
Qy	645	PheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAla	664	Db	3002	CACAGCCTGTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTSCACCAACATCTAC	3061
Db	1922	TTTCATCCCAAGCTGACGGCTGCGGCCGATGTTGAACATGGACTACGTCTGGGGAGCC	1981	Qy	1025	LysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHis	1044
Qy	665	ArgThrPheArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPhe	684	Db	3062	AAGATCCTCTGCTGACAGGCTACAGGTTTTCAGCATGTGTGTGTCAGCTCCCATTTTCAT	3121
Db	1982	AGAACGTTCCGACAGAAAAAGGGCGAGCGTCTCACCTCGAGGGTGAAGGCACCTGTC	2041	Qy	1045	GlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeu	1064
Qy	685	SerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGly	704	Db	3122	CAGCAAGTTTGAAGAACCCACCATTTTCTGCGCGTCACTCTGACACGGCTCTCCCTC	3181
Db	2042	AGCGTGTCAACTACGAGGGGCGGGCGCCCGGCTCTTGGGCGCTCTGTGCTGGG	2101	Qy	1065	CysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGlyAlaAla	1084
Qy	705	LeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAspPro	724	Db	3182	TGCTACTCCATCTCTGAAAGCAAGAACGACGAGGATGTGCTGGGGGCCAAGGGCGCCGC	3241
Db	2102	CTGGACGATATCCACAGGGCTGCGCGACCTTCGTGCTGCTGCGGGCCAGGACCCG	2161	Qy	1085	GlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeuLysLeu	1104
Qy	725	ProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIleProGln	744	Db	3242	GGCCCTCTGCCCTCCGAGCGCGTGACGTGGCTGTGCCACCAAGCATTTCTTGTCTCAAGCTG	3301
Db	2162	CCGCTCAGCTGTACTTTGTCAAGTGGATGTGACGGGCGCGTACGACACCATCTCCCCAG	2221	Qy	1105	ThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGln	1124
Qy	745	AspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysValArg	764	Db	3302	ACTCGACACCGTGTACCTACGTGCCACTCTCTGGGGTCACTCAGGACAGCCCGACGACG	3361
Db	2222	GACAGGCTCAGGAGGTTCATCGCCAGCATCATCAAAACCCAGAACACGTACTGCGTCCGT	2281	Qy	1125	LeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsnProAla	1144
Qy	765	ArgTyrAlaValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHis	784	Db	3362	CTGAGTCGGAAGCTCCCGGGAGACGACGCTGACTGCCCTGAGGGCGCGACCAACCCGCA	3421
Db	2282	CGGTATCCGTGTCAGAGAGGCCGCCATGCGGCACGCTCCGCAAGGCTTCAAGAGCCAC	2341	Qy	1145	LeuProSerAspPheLysThrIleLeuAsp	1154
Qy	785	ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGlu	804				

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Db      3422 CTGCCCTCAGACTTCAAGACCATCTCGGAC 3451
RESULT 12
US-09-749-728B-32
; Sequence 32, Application US/09749728B
; Patent No. US20020142457A1
; GENERAL INFORMATION:
; APPLICANT: Umezawa, Akihiro
; APPLICANT: Hata, Jun-ichi
; APPLICANT: Fukuda, Keiichi
; APPLICANT: Ogawa, Satoshi
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Gojo, Satoshi
; APPLICANT: Yamada, Yoji
; TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOMY
; FILE REFERENCE: 00766.000043
; CURRENT APPLICATION NUMBER: US/09/749,728B
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: H11-372826
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: PCT-JP00-01148
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: PCT-JP00-07741
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver.2.0
; SEQ ID NO 32
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: (1)..(3399)
US-09-749-728B-32

Alignment Scores:
Pred. No.:      0      Length:      3396
Score:          5961.00      Matches:      1132
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      98.06%      Indels:      0
DB:               10      Gaps:        0

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Qy      43 ValLeuProLeuAlaThrPheValArgLeuGlyProGlnGlyTyrArgLeuValGln 62
Db      61 GTGCTGCCGTGGCCACGTTCTGGCGCGCTGGGGCCCGCAGGGCTGGCGCTGGTGCAG 120
Qy      63 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 82
Db      121 CGCGGGGACCGCGGGCTTTCCGGCGCTGGTGGCCAGTGCCTGTGTGGTGGCTGGCTGG 180
Qy      83 AspaAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 102
Db      181 GAGCGACGGCGCGCGCGCGCGCGCTCTCCGCCAGGTGCTCCGCCAGGAGAGAGAGAGAG 240
Qy      103 ValAlaArgValLeuGlnArgLeuCysGluArgGlyProGlnGlyAlaLysAsnValLeuAlaPheGly 122
Db      241 GTGGCCGAGTGTGCAGAGGCTGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Qy      123 PheAlaLeuLeuAspGlyAlaArgGlyGlyProGlnGlyAlaPheThrThrSerValArg 142
Db      301 TTGGCGCTGTGCAGCGGGCGCGCGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Qy      143 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeu 162
Db      361 AGCTACTGCGCCCAACACGGGTGACCGACGCTCGGGGGAGCGGGCGGTGGGGGCTGCTG 420

163 LeuArgArgValGlyAspValLeuValHisLeuLeuAlaAlaArgCysAlaLeuPheVal 182
Db      CTGCGCGCGCTGGCGGACGACGTGCTGCTCACCTGCTGGCAGCGTGGCGGCTCTTTGTG 480
Qy      183 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 202
Db      CTGGTGGCTCCAGCTGCGCTACCAAGTGTGCGGCGCGCGCTGTACAGCTCGCGCT 540
Qy      203 AlaThrGlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 222
Db      GCCACTCAGCGCGCGCGCGCGCGCGCTAGTGAGCCCGCGCGCGCGCTGGGATGCCAA 600
Qy      223 ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 242
Db      CGGGCTGGAACCATAGCTCAGGAGCGCGGGGTCCCGCTGGGCTGCCAGCCCGGGT 660
Qy      243 AlaArgArgGlyGlySerAlaSerArgSerLeuProLeuProGlyArgProArgArg 262
Db      GCGAGGAGCGCGGGGCGAGTCCAGCGCAAGTCTGCGGTTGCCCAAGAGGCCAGCGGT 720
Qy      263 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrAlaHisProGly 282
Db      GCGCTGCCCTGAGCGGAGCGGCGCGCTGGGCGAGGGTCTGGGCGCGCGCGCGCG 780
Qy      283 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 302
Db      AGGACGCGTGACCGAGTGACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Qy      303 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 322
Db      GAGCCACCTCTTTGGAGGGTGGCTCTCTGGCAGCGCGCTCCCTGCCAGCCCGCGCA 840
Qy      323 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProProTyrAspThrPro 342
Db      CGCCAGCACACGCGGGCGCGCGCGCTCCACATCGCGCGCGCGCGCGCGCGCGCGCG 960
Qy      343 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 362
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Qy      363 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 382
Db      CTGGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
Qy      383 ValGluThrIlePheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro 402
Db      GTGGAGACCATCTTCTGGGTTCAGGCGCTGGATGCCAGGACTCCCGCGAGGTGGCC 1140
Qy      403 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuGlyAsnHis 422
Db      CGCGTGGCGCGCGCGCTACTGGCAATGCGCGCGCTGTCTCTGTGAGCTGTCTGGGACCCAC 1200
Qy      423 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 442
Db      GCGCAGTGGCGCGCTACGGGGGTCTCTCAAGACGACGTGCGCGCTGCGAGCTGCGGTCA 1260
Qy      443 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 462
Db      CCAGCAGCGGTGTCTGTGGCGGAGAGCGCGCGCGCGCTGTGGGGCGCGCGCGCGCG 1320
Qy      463 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 482
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Qy      483 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 502
Db      GTGTACGGCTGTGGTGGCGGCTGTGCTGCGCGGTGTGGTGGCGCGCGCGCGCGCGCG 1440
Qy      503 ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 522
Db      AGGCACACACGCGCGCTCTCTCAGGACACACCAAGAGGTTCATCTCTCCCGGGGAGCAT 1500
Qy      523 AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 542
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Db	1501	GCCAAAGCTCTCGCTGCAAGAGCTGACGTGAAGATGAGCTGCGGGACTGCGCTTGCGTG	1560
Qy	543	ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle	562
Db	1561	CGCAGGAGCCAGGGGTGGCTGTGTTCCGGCCGCAGACACCGCTGCGCTGAGGAGATC	1620
Qy	563	LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe	582
Db	1621	CTGGCCAAAGTTCCCTGCACTGCTGATCAGTGTGTACCTGCTCGAGCTGCTCAGGTCTTTC	1680
Qy	583	PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal	602
Db	1681	TTTTTATGTCAGGAGACAGCTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGC	1740
Qy	603	TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu	622
Db	1741	TGGAGCAAGTTGCAACACATTTGNAATCAGACAGCACTTTGAAGAGGTGACGTGCGGGAG	1800
Qy	623	LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	642
Db	1801	CTGTGCGAAGCAGAGGTTCAGCAGCATCGGAGCCAGCCAGCGCCCTGCTGACGTCCAGA	1860
Qy	643	LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal	662
Db	1861	CTCCGCTTCATCCCAAGCTGACGGGCTCGGCCGATTTGTAACATGAGTACGTGCTG	1920
Qy	663	GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	682
Db	1921	GGAGCCAGACGTTCCGCAGAAAGAGCGCCGAGCGTCTCACCTCGAGGGTGAAGGCA	1980
Qy	683	LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal	702
Db	1981	CTGTTCAGCGTGTCAACTACGAGCGCGCGCGCCGCTCTCTGCGCGCTCTGCTG	2040
Qy	703	LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln	722
Db	2041	CTGGGCTGAGCAGATATCCACAGGGCTGCGCACCTTCGTGCTGCGTGTGCGGGGCCAG	2100
Qy	723	AspProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle	742
Db	2101	GACCGCGCGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGCGGTGACGACACCATC	2160
Qy	743	ProGlnAspArgLeuThrGluValIleAlaSerIleLysProGlnAsnThrTyrCys	762
Db	2161	CCCCAGACAGCTCACGGAGTTCATCGCCAGCATCATCAACCCCAAGACACGTAATGC	2220
Qy	763	ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys	782
Db	2221	GTGGCTCGGTATGCGGTGTCAGAGAGCGCCCATGGGCACGTCCCAAGGCGCTTCAG	2280
Qy	783	SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu	802
Db	2281	AGCCACGCTCTACTTTGACAGACCTCCAGCGGTACATGCGACAGTCTGCTGCTCACCTG	2340
Qy	803	GlnGluThrSerProLeuArgAspAlaValIleGlnSerSerSerLeuAsnGlu	822
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Qy	823	AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIle	842
Db	2401	GCCAGCAGTGGCTCTTCGACGCTTCTTACGCTTCATGTGCCACACGCGGTGCGCATC	2460
Qy	843	ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	862
Db	2461	AGGGCAAGTCTTACGTCCAGTCCAGGGATCCCGCAGGGCTTCATCTCTCCACGCTG	2520
Qy	863	LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp	882
Db	2521	CTCTGCAGCTGTGCTACGGCGACATGAGACAAGCTGTTTGGGGGATTCGGCGGAC	2580
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; LENGTH: 3453	
; TYPE: DNA	
; ORGANISM: Homo sapiens	
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Score:	5952.00
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Best Local Similarity:	99.82%
Mismatches:	1
Query Match:	97.91%
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Gaps:	0
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QY	23 MetProArgAlaProArGcYsArgAlaValaArgSerLeuLeuArgSerHisTrArGlu 42
DB	10 ATGCGCGGCGCTCCCGCTGCGAGCGCTGCGCTGCCCTGCTGCGACCGCACTACCGCGAG 69
QY	43 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrArGLeuValGln 62
DB	70 GTGCTGCGGCTGCCACGTTCTGTCGGCGGCTGGGGCCCCAGGGCTGGCGCTGGTGCAG 129
QY	63 ArgGlyAspProAlaAlaPheArgAlaLeuValaGlnCysLeuValCysValProTrp 82
DB	130 CCGGGGACCGCGGCGCTTCCGCGCGCTGTGTGCCAGTCGCTGGTGTGCTGGCTGGCTGG 189
QY	83 AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 102
DB	190 GAGCGACGGCGCCCCCGCGCCCTTCCTCCGCGAGGTGCTGCCCTGAAGGAGCTG 249
QY	103 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 122
DB	250 GTGGCCGAGTGCTGCACAGGCTGTGCGAGCGCGCGGAAGAACGTGCTGGCTTCGGC 309
QY	123 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrSerValArg 142
DB	310 TTCGCGCTGCTGAGCGGGCGCGGGGGCCCCCGCGAGGCTTCACACACAGCGTGGC 369
QY	143 SerTyLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu 162
DB	370 AGCTACCTGCCACACACGCTGACGACGACCTCGGGGGAGCGGGGCTGGGCTGCTG 429
QY	163 LeuArgArgValGlyAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 182
DB	430 CTGCGCGCGTGGGCGACGAGCTGCTGTTTCCACCTGCTGGCACGCTGGCGGCTTTTGTG 489
QY	183 LeuValAlaProSerCysAlaTyGlnValCysGlyProProLeuTyGlnLeuGlyAla 202
DB	490 CTGGTGGCTCCAGCTGGCGCTTACAGGTGTGTCGGGCGCGCGCTTACCAAGCTCGGCGCT 549
QY	203 AlaThrGlnAlaArgProProHisAlaSerGlyProArgArgLeuGlyCysGlu 222
DB	550 GCCACTAGCGCGCGCGCGCGCGCGCTAGTGGACCCCGAAGGGGCTGTGGATCGGAA 609
QY	223 ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 242
DB	610 CGGGCTTGAACCATAGGCTCAGGAGCGCGGGGTCCCCCTGGGCTGCCAGCCCCGGGT 669
QY	243 AlaArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 262
DB	670 GCGAGAGGCGCGGGGGCAGTGCCAGCGGAAGTCTGCCCTTGCCCAAGAGGCCACGCGCT 729
QY	263 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly 282
DB	730 GCGCTGCCCTGAGCGGAGCGACCGCGCTTGGCGAGGGGTCTTGGCGCCACCGCGGC 789
QY	283 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 302
DB	790 AGGACGCTGGACCGAGTGACCGTGGTTCTGTGTGTGTCTCACTGCCAGACCCCGCGAA 849
QY	303 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 322

Db	850	GAAGCCACCTCTTTGGAGGGTGCCTCTCTGGCACACGCCACCTCCACCCATCGTGGGC	909
QY	323	ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProThrPaspThrPro	342
Db	910	CGCCAGACACACCGGGGCCCCCATCCACATCGCGGCACACAGTCTCTCTGGACACGCCT	969
QY	343	CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln	362
Db	970	TGTCCCGGGTGACGCGGACCAAGCACTTCTCTACTCTCTACGCGGACACAGGACGAG	1029
QY	363	LeuArgProSerPheLeuLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	382
Db	1030	CTGGGGCCCTCTTCCTACTCAGCTCTCTGAGGCCACGCTGAGTGCCTCGCTCGAGGCTC	1089
QY	383	ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	402
Db	1090	GTGGAGACCAVCTTTCTGGGTTCAGGCCCTGGATGCCAGGGACTCCGCCACAGTGTGCC	1149
QY	403	ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis	422
Db	1150	CGCCTGCCCCACGCGTACTGGCAATCGGCCCTCTTCTTGGAGCTGCTTGGGAACCA	1209
QY	423	AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	442
Db	1210	CGCAGTGGCCCTACGGGGTCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTCAACC	1269
QY	443	ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	462
Db	1270	CCAGCAGCCGGTGCTGTGCGCGGGAAGACCCACGGGCTCTGTGGCGGCCCCCGAGGAG	1329
QY	463	GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln	482
Db	1330	GAGGACACAGNCCCGCTGCGCTGGTCGACTGCTCGCCAGCACACGCCCTGTCGAG	1389
QY	483	ValTyrGlyPheValArgAlaCysLeuArgLeuValProProGlyLeuThrPrgLys	502
Db	1390	GTGTACGGCTTGTGTGCGGGCTGCTCGCGGGCTGTGTGCCACAGGCCCTCTGGGGCTCC	1449
QY	503	ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	522
Db	1450	AGGCACAACCAACGCCGCTTCTTCAGGAACACCAAGAAGTTCATCTCTCTGGGGGAAGCAT	1509
QY	523	AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu	542
Db	1510	GCCAAGCTCTCGTCGAGGAGTGCAGTGTGAAGATGAGCGTGGCGGACTCGCTTGGCTG	1569
QY	543	ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle	562
Db	1570	CGCAGGAGCCAGGGGTGTGCTGTGTCCGGCCGACAGCACCGTCTGCTGTAGGAGATC	1629
QY	563	LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe	582
Db	1630	CTGGCCCAAGTTCCTGCAGCTGGCTGATGAGTGTGTACGTCGTCAGTGTCTCAGTCTTTC	1689
QY	583	PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal	602
Db	1690	TTTTTATGTACGGAGACACGTTTCAAAAGACAGGCTCTTTTTCTACCGCCGCGATGTC	1749
QY	603	TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu	622
Db	1750	TGGAGCAAGTTGCAAGCATTTGAAATCAGACAGCACTTTGAAGAGGTGTCAGCTGCGGGAG	1809
QY	623	LeuSerGluAlaGluValArgGlnHisArgGluAlaAArgProAlaLeuLeuThrSerArg	642
Db	1810	CTGTGGAAGCAGAGGTTCAGCGAGCATCGGGAAGCCAGGCCGCCCTGCTGACGTCACGA	1869
QY	643	LeuArgPheIleProLysProAspGlyLeuArgProfileValAsnMetAspTyrValVal	662
Db	1870	CTCGCTTCATCCCAAGCCTGACGGGCTCGGGCCGATTTGTGAACATGGACTACGTCGTG	1929
QY	663	GlyAlaAargThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	682
Db	1930	GGAGCCAGAAGCTTCGCGACAGAAAGAGGGCCGAGCTCTCTACCTCGAGGTGAGGCA	1989



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QY 683 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 702
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QY 723 AspProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 742
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QY 783 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 802
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QY 843 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 862
Db 2470 AGGGGCAAGTCTACGTCCAGTCCAGGAGTCCCGCAGGGTCCATCTCTCCAGCGTG 2529
QY 863 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 882
Db 2530 CTCTGAGCCTGTGCTACGGCAGCATGGAGAACAGCTCTTCGGGGGATTCGGCGGGAC 2589
QY 883 GlyLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 902
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QY 903 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 922
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QY 923 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 942
Db 2710 CGGAAGACAGTGGTGAACCTCCCTGTAGAGACGAGGCCCTGGGTGGCAGCGCTTTGTT 2769
QY 943 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 962
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QY 963 GluValGlnSerAspTyrSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 982
Db 2830 GAGGTGCAGGAGGACTACTCCAGTATGCCGAGCCTCCATCAGAGCCAGTGTCACTTC 2889
QY 983 AsnArgGlyPheIysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 1002
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QY 1003 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1022
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QY 1023 IleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1042
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QY 1063 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1082
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QY 1103 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1122
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QY 1123 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1142
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RESULT 14
US-10-105-616-1
; Sequence 1, Application US/10105616
; Publication No. US20030175967A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Clark, A. J.
; APPLICANT: Denning, Chris
; APPLICANT: Cui, Wei
; APPLICANT: Zhao, Debbiao
; TITLE OF INVENTION: Vectors for Telomerizing Nuclear Donor Cells and Improving the
; TITLE OF INVENTION: of Nuclear Transfer
; FILE REFERENCE: 732/002
; CURRENT APPLICATION NUMBER: US/10/105,616
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US Provisional Application 60/277,749
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 13766
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial construct comprising human TERT, myeloproliferative
; OTHER INFORMATION: rcoma virus (MPSV) promoter, and vector components
US-10-105-616-1
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Alignment Scores:
Pred. No.: 0 Length: 13766
Score: 5952.00 Matches: 1130
Percent Similarity: 99.91% Conservative: 1
Best Local Similarity: 99.82% Mismatches: 0
Query Match: 97.91% Indels: 1
DB: 12 Gaps: 0

US-08-951-733-20 (1-1154) x US-10-105-616-1 (1-13766)
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QY 43 ValLeuProLeuAlaThrPheValArgLeuGlyProGlnGlyTrpArgLeuValGln 62
Db 4049 GTGCTCCGCTGGCCACGTTCGTGGCGGCCCTGGGGCCCCAGGGCTGGCGGTGGTGCAG 4108
QY 63 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 82
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QY	103	VallAlaArgValLeuLeuGlnArgLeuCysGluArgGlyAlaLysAanValLeuAlaPheGly	122
DB	4229	GTGGCCCGAGTGTCTGACAGAGCTGTGCGAGCGCGCGGGAAGACGTGCTGGCCCTTCGGC	4288
QY	123	PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluLaLaPheThrThrSerValArg	142
DB	4289	TTCCGCGTGTCTGGACGGGGCCCGCGGGGGCCCCCGGAGGCCTTCACACACAGCGTCGCG	4348
QY	143	SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrrpGlyLeuLeu	162
DB	4349	AGCTACCTTCCCAACACGGTGACCGACGTGCGGGGGAGCGGGGGCGTGGGGCGTGTG	4408
QY	163	LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal	182
DB	4409	CTGCGCGCGTGGGCGAGCGTGTCTGGTTACCTGTGTGGACGCTCGCGCGCTCTTTGTG	4468
QY	183	LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla	202
DB	4469	CTGTGGCTCCACGCTCGGCTACAGGTGTGGGGCGCGCGCTGTACACAGCTCGCGCT	4528
QY	203	AlaThrGlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu	222
DB	4529	GCCACTCAGGCCCGGCCCGCCACACGCTAGTGGACCCCGGAAGGCGTGTGGGATGCGAA	4588
QY	223	ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly	242
DB	4589	CGGGCCTGGAAACCATAGCGTCAGGAGCGCGGGTCCCTCGGCGCTGCCAGCCCGGGT	4648
QY	243	AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg	262
DB	4649	GCGAGGAGCGCGGGGCGAGTGCAGCGGAAGTCTGCGCTTGGCCAAAGAGGCCCGACGCGT	4708
QY	263	GlyAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly	282
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QY	283	ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu	302
DB	4769	AGGACGCGTGGACCGAGTGCCTGGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	4828
QY	303	GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	322
DB	4829	GAAGCCACCTCTTTGGAGGTGCGCTCTCTGGACACGCGCCACTCCACCCATCCGTGGGC	4888
QY	323	ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro	342
DB	4889	CGCCAGCACACCGGGGCCCGCCCATCATCGCGGCCACCGCTCCCTGGGACACGCGCT	4948
QY	343	CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln	362
DB	4949	TGTCCCGCGGTGTACGCGAGACCAAGCACTTCTCTACTCTCAGCGCACAAGGAGCAG	5008
QY	363	LeuArgProSerPheLeuLeuSerLeuArgProSerLeuThrGlyAlaArgArgLeu	382
DB	5009	CTCGGGCCCTCTCTCTACTACTACTCTCTGAGGCCACGCGCTGACTGGCGCTCGGGAGCTC	5068
QY	383	ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	402
DB	5069	GTGAGACCATCTTTCTGGGTCCAGGCCCTGGATGCCAGGGACTCCCCCGCAGGTGTGCC	5128
QY	403	ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuGlyAsnHis	422
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QY	443	ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	462
DB	5249	CCAGCAGCGGTGTCTGTGCGCGGAGAAAGCCAGGGCTGTGTGGGGCCCCCGAGGAG	5308
QY	463	GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln	482
DB	5309	GAGGACACAGACCCCGCTGGTGGAGCTGTCTCGCGCAGCACAGACGCCCTGGCAG	5368
QY	483	ValTYrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTYrGlySer	502
DB	5369	GNGTACGGCTTCGTGGGGCTCGCTGGCGGGCTGGTGGCCCCAGGCCCTCGGGGCTCC	5428
QY	503	ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	522
DB	5429	AGGCCAAACGAACGCGCTTCTCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGAGCAT	5488
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QY	543	ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle	562
DB	5549	CGCAGGACCCAGGGTGGCTGTGTCCGGCCGACAGCACCGCTGTGGTGAGGAGATTC	5608
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DB	5609	CTGGCCAAAGTTCCTGCACTGGCTCATCAGTGTGTACGTCTCGAGCTGCTCAGGCTTTTC	5668
QY	583	PheTYrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTYrArgLysSerVal	602
DB	5669	TTTATTATGTACGGAGACACGTTTCAAAAGAACAGGCTCTTTTCTACCGGGCGAGTGT	5728
QY	603	TrpSerLysLeuGlnSerIleGlyLeArgGlnHisLeuLysArgValGlnLeuArgGlu	622
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QY	623	LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	642
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QY	643	LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTYrValVal	662
DB	5849	CTCCGCTTCATCCCCAAGCCTGACGGCTCGGCCCATGTTGAACATGACACTACGCTCGTG	5908
QY	663	GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	682
DB	5909	GGAGCCAGAGTTCCGCACAGAAAGAGGGCCGACGGTCTCACCTCGAGGGGTGAAGCCA	5968
QY	683	LeuPheSerValLeuAsnTYrGluArgAlaArgProGlyLeuLeuGlyAlaSerVal	702
DB	5969	CTGTTCAGCTGTCTCAACTACGAGCGGGCGCGGCCCTCTCTGGGGCCCTCTGTG	6028
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DB	6029	CTGGGCTTGACGATATCCACAGGGCTGGCGCACCTCTGTGTGCTGTGGGGGCCCGAG	6088
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DB	6089	GACCCCGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGGCGGTACACACCATC	6148
QY	743	ProGlnAspArgLeuThrGluValIleAlaSerIleLysLysProGlnAsnThrTYrCys	762
DB	6149	CCCCAGCACAGGCTCAGGGAGGTTCATCGCCAGCATCATCAACCCCCAGACACTACTGCC	6208
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DB	6209	GTGGCTCGGTATGCGCTGTGTTCCAGAGAGCGGCCCATGTCGTCGCTCGCAAGGCCCTCAAG	6268
QY	783	SerHisValSerThrLeuThrAspLeuGlnProTYrMetArgGlnPheValAlaHisLeu	802
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; Publication No. US20030175967A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Clark, A. J.
; APPLICANT: Denning, Chris
; APPLICANT: Cui, Wei
; APPLICANT: Zhao, Debbiao
; TITLE OF INVENTION: Vectors for Telomerizing Nuclear Donor Cells and Improving the
; FILE REFERENCE: 732/002
; CURRENT APPLICATION NUMBER: US/10/105,616
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US Provisional Application 60/277,749
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 8742
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial construct comprising human TERT, myeloproliferative
; US-10-105-616-6
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Score: 5925.00 Matches: 1129
Percent Similarity: 99.82% Conservative: 1
Best Local Similarity: 99.73% Mismatches: 2
Query Match: 97.47% Indels: 1
DB: 12 Gaps: 0
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QY 83 AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 102
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QY 203 AlaThrGlnAlaArgProProHisAlaSerGlyProArgArgLeuGlyCysGlu 222
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Qy	463	GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln	482
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Qy	523	AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu	542
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Qy	543	ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluIle	562
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Copyright (c) 1993 - 2003 CompuGen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	3784.4	99.6	4015	10	US-09-990-080-1	Sequence 1, Appli
3	3784.4	99.6	4015	10	US-09-843-676-224	Sequence 224, App
4	3784.4	99.6	4015	10	US-09-953-052-1	Sequence 1, Appli
5	3784.4	99.6	4015	14	US-10-053-758-224	Sequence 224, App
6	3784.4	99.6	4015	14	US-10-053-758-224	Sequence 1, Appli
7	3784.4	99.6	4015	14	US-10-208-243-1	Sequence 224, App
8	3784.4	99.6	4015	14	US-10-054-295-224	Sequence 1, Appli
9	3784.4	99.6	4015	14	US-10-054-611-224	Sequence 224, App
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12	3618.6	95.3	4029	10	US-09-843-676-173	Sequence 173, App
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14	3618.6	95.3	4029	14	US-10-053-758-173	Sequence 173, App
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21	3396	89.4	3396	US-09-749-728B-32	Sequence 32, Appl
22	3388	89.2	8742	US-10-105-616-6	Sequence 6, Appl
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## ALIGNMENTS

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RECORD 1
US-09-733-294A-3
; Sequence 3, Application US/09733294A
; Patent No. US20020045588A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
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; TYPE: DNA
; ORGANISM: Homo sapiens
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 3781 CCAGAT 3786

RESULT 2
US-09-990-080-1
; Sequence 1, Application US/09990080
; Patent No. US20020102686A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 018/258C
; CURRENT APPLICATION NUMBER: US/09/990,080
; PRIOR FILING DATE: 1998-08-03
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA
US-09-990-080-1

Query Match 99.6%; Score 3784.4; DB 10; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 121 GCGCGTCCCGCTGCGCAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGCTGCT 180
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Db	301	CCGAGTGTGACAGAGGTGTGCGAGCGCGCGCAAGAAAGTGTGCTGCCCTTCGGCTTCGC	360
QY	373	GCTGCTGGAGGGGCCCGCGGGGGCCCGCCCGAGGCCCTTCAACACACAGCTGTGCCAGCTA	432
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QY	433	CCTGCCAACACAGTGTACCGACGACACTGCGGGGAGCGGGGCTGGGGCTGCTGCTGGC	492
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QY 3673 GAGTGTCCAGCACACCTGCCGCTTTCACCTTCCACAGGCTGGCGCTCGGCTCCACCCCA 3732  
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QY 3793 CCTGAT 3798  
Db 3781 CCAGAT 3786

## RESULT 3

US-09-843-676-224  
; Sequence 224, Application US/09843676  
; Patent No. US20020164786A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: NO. US20020164786A1el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/843,676  
; FILING DATE: 26-Apr-2001  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US/08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US/08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US/08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 224:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4015 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

:	TOPOLOGY: linear
:	MOLECULE TYPE: cDNA
:	FEATURE:
:	NAME/KEY: CDS
:	LOCATION: 56..3454
:	OTHER INFORMATION: /product= "hTERT"
:	/note= "human telomerase reverse
:	transcriptase (hTERT) catalytic protein
:	component"
:	SEQUENCE DESCRIPTION: SEQ ID NO: 224:
:	US-09-843-676-224
	Query Match 99.6%; Score 3784.4; DB 10; Length 4015;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	13 GCAGCGTCGCTCCTGCTGGCCAGCGTGGAAGCCCTGGCCCGGCCACCCC CGCATGCC 72
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QY	61 GCGCGCTCCCGCGTCCGAGCGGTGCCTCCCTGTCGCGCAGCCACTACCGCGAGGTGCT 120
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QY	133 GCCGCTGGCACAGTTGTCGGCGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGCAAGCGGG 192
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QY	301 CCGAGTCTGCAGAGGTGTGCGAGCGGCGCGAAGAACGTGTGGCTTCGGCTTCGC 360
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QY	373 GTCTGTGACGGGGCCGCGGGGCCCCCGAGGCTTACCACACAGGTCGCGAGCTA 432
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QY	361 GTCTGTGACGGGGCCGCGGGGCCCCCGAGGCTTACCACACAGGTCGCGAGCTA 420
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QY	421 CCTGCCAACACGGTGACCGACACTGCGGGGAGCGGGGCGTGGGGCTGCTCTGGC 480
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QY	481 CCGGCTGGGGACAGCTGTCTGTTACCTGCTGGCAGCTGCGGCGCTTTTGTGCTGGT 540
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QY	553 GGCTTCCAGCTGCGCCTACCAAGTGTGGGGCCCCGCTGTACCAGCTCGGGCTGCCAC 612
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QY	541 GGCTTCCAGCTGCGCCTACCAAGTGTGGGGCCCCGCTGTACCAGCTCGGGCTGCCAC 600
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QY	661 CTGGAACCATAGCGTCAAGGAGGCCGGGTCCCCCTTGGGCTTGCACGCCGGGTGCGAG 720
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QY	781 TGGCCCTTGACCGGAGCGGACGCCGTTTGGGACGGGTTCCTGGGCCACCGCGGAGAC 840
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QY	853 GCGTGGACCGAGTGACCGTGGTTCTCTGTGTGGTGTCACTGCCAGACCCGCGGAAGAC 912
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Db 1921 CTTTCATCCCAAGCCTGACGGGCTCGGCCGATTCTGAACATGGACTACGTCGTGGGAGC 1980  
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Db 1981 CAGAACCTTCCGCAGAGAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTT 2040  
QY 2053 CAGCGTGTCAACTACGAGCGGGCCGCGGCCCGCCGCTCTGCGGCGCTCTGCTCTGGG 2112  
Db 2041 CAGCGTGTCAACTACGAGCGGGCCGCGGCCCGCCGCTCTGCGGCGCTCTGCTCTGGG 2100  
QY 2113 CTTGACGATATCCACAGGGCTTGGCGACCTTCCTGCTGTGCTGTGCGGGCCAGGACCC 2172  
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QY 2173 GCCGCTGAGCTGTACTTGTCAAGGTGATGTAGGGGGGCTGAGACACATCCCGCA 2232  
Db 2161 GCCGCTGAGCTGTACTTGTCAAGGTGATGTAGGGGGGCTGAGACACATCCCGCA 2220  
QY 2233 GGACAGGCTCAGGAGGTTCATCGCCAGCATCATCAAAACCCAGAACAGTACTGCTGGG 2292  
Db 2221 GGACAGGCTCAGGAGGTTCATCGCCAGCATCATCAAAACCCAGAACAGTACTGCTGGG 2280  
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QY 2473 CAGTGGCTCTTTCGACGCTTCTTCTACGCTTCATGTGCCACACGCGTGGCATCAGGGG 2532  
Db 2461 CAGTGGCTCTTTCGACGCTTCTTCTACGCTTCATGTGCCACACGCGTGGCATCAGGGG 2520  
QY 2533 CAAGTCTTACGTCAGTCCAGGGATCCCGAGGGCTCCATCTCTCAGCGTCTCTG 2592  
Db 2521 CAAGTCTTACGTCAGTCCAGGGATCCCGAGGGCTCCATCTCTCAGCGTCTCTG 2580  
QY 2593 CAGCTGTGCTACGCGACATGAGAACAAAGCTGTTTGGGGATTCGGCGGAGCGGCT 2652  
Db 2581 CAGCTGTGCTACGCGACATGAGAACAAAGCTGTTTGGGGATTCGGCGGAGCGGCT 2640  
QY 2653 GCTCTGCTGTGTTGATGATTTCTTGTGTGACACCTCACCTCACCCACGCGAAAC 2712  
Db 2641 GCTCTGCTGTGTTGATGATTTCTTGTGTGACACCTCACCTCACCCACGCGAAAC 2700  
QY 2713 CTTCTCAGGACCTTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTGAACCTTCGGAA 2772  
Db 2701 CTTCTCAGGACCTTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTGAACCTTCGGAA 2760  
QY 2773 GACAGTGTGAATTCCTCTGAGAGACGAGGCTTGGTGGCGAGGCTTGTTCAGAT 2832  
Db 2761 GACAGTGTGAATTCCTCTGAGAGACGAGGCTTGGTGGCGAGGCTTGTTCAGAT 2820  
QY 2833 GCCGCGCCACGCGCTATTCCCTGCTGGTGGCGCTGCTGTGATACCCGACCCCTGGAGT 2892  
Db 2821 GCCGCGCCACGCGCTATTCCCTGCTGGTGGCGCTGCTGTGATACCCGACCCCTGGAGT 2880  
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QY 2953 CGGCTTCAAGCTGGGAGAACATGCGTCGAAACTCTTGGGGTTCGGGCTGAAGT 3012  
Db 2941 CGGCTTCAAGCTGGGAGAACATGCGTCGAAACTCTTGGGGTTCGGGCTGAAGT 3000  
QY 3013 TCACAGCTGTTTCTGGATTTGAGGTGAACAGGCTCCAGAGCGTGTGCACCAACATCTA 3072  
Db 3001 TCACAGCTGTTTCTGGATTTGAGGTGAACAGGCTCCAGAGCGTGTGCACCAACATCTA 3060

QY 3073 CAAGATCTCTCTGCTGACAGGCTACAGGTTTCACGCATGTGTGCTGACAGTCCCATTTCA 3132  
Db 3061 CAAGATCTCTCTGCTGACAGGCTACAGGTTTCACGCATGTGTGCTGACAGTCCCATTTCA 3120  
QY 3133 TCAGCAAGTTTGGAGAAACCCACACATTTTCTGCGCGTCATCTCTGACACGCGCTCCCT 3192  
Db 3121 TCAGCAAGTTTGGAGAAACCCACACATTTTCTGCGCGTCATCTCTGACACGCGCTCCCT 3180  
QY 3193 CTGTACTCTCCCTGAAAGCCAAAGACGAGGATGTGCTGGGGCCAAAGGGCGCGC 3252  
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Db 3301 GACTCGACACCGTGTCACTAGCTGCTCCTCTGGGTGCTCAGGACAGCCACAGCGCA 3360  
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QY 3433 ACTGCCCTCAGACTTCAAGACCATCTGACTGTATGGCCACCCGCCACAGCCAGGCGCA 3492  
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGACTGTATGGCCACCCGCCACAGCCAGGCGCA 3480  
QY 3493 GAGCAGACACCAAGCGCTGTACGCGGGCTCTACGTCGCCGGCTCTACGTCGCCAGGAGGGGGCGC 3552  
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QY 3793 CTTGAT 3798  
Db 3781 CCAGAT 3786

## RESULT 4

US-09-953-052-1

; Sequence 1, Application US/09953052

; Patent No. US20020173476A1

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin B.

; Andrews, William H.

; TITLE OF INVENTION: Antisense Compositions for Detecting and

; Inhibiting Telomerase Reverse Transcriptase

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 09/09/953,052  
FILING DATE: 14-Sep-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052,919  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/974,549  
FILING DATE: 19-NOV-1997  
APPLICATION NUMBER: US 08/974,584  
FILING DATE: 19-NOV-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Parent, Annette S.  
REGISTRATION NUMBER: 42,058  
REFERENCE/DOCKET NUMBER: 015389-003600US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4015 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 56..3454  
OTHER INFORMATION: /product= "human telomerase reverse transcriptase (hTRT)"  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Query Match 99.6%; Score 3784.4; DB 10; Length 4015;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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1021 CCGGGTGTACCGGAGACCAAGCACTTCTTCTACTCTCCTCAGGGGACAGGAGGAGGCTGGC 1080  
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QY  
1153 GACCATCTTCTGGGTTCCAGGGCCCTGGATGCCAGGAGTCCCGCGAGGTGGCCCGCT 1212  
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1141 GACCATCTTCTGGGTTCCAGGGCCCTGGATGCCAGGAGTCCCGCGAGGTGGCCCGCT 1200  
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DB	1261	GTGCCCCACGGGTCCTCCTCAAGACGACTGCCGCTGCGAGCTGCGGTCAACCCACG	1320
QY	1333	AGCCGGTGTCTGTGTCGCCGGAGAACCCAGGGCTCTGTGGCGGCCGCCGAGGAGGAGGA	1392
DB	1321	AGCCGGTGTCTGTGTCGCCGGAGAACCCAGGGCTCTGTGGCGGCCGCCGAGGAGGAGGA	1380
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DB	1381	CACACACCCCGTGCCTGGTGGTACAGTGTGCGGCACACAGACAGCCCTTGGCAGGTGTA	1440
QY	1453	CGGCTTCGTGCGGGCTGCCTGCGCGCGCTGGTGCCTCCAGGCTCTGGGGCTCCAGGCA	1512
DB	1441	CGGCTTCGTGCGGGCTGCCTGCGCGCGCTGGTGCCTCCAGGCTCTGGGGCTCCAGGCA	1500
QY	1513	CAACGAACCGCGCTTCCTCAGGAACACCAAGAAGTTTCATCCCTGGGGAAAGCATGCCAA	1572
DB	1501	CAACGAACCGCGCTTCCTCAGGAACACCAAGAAGTTTCATCCCTGGGGAAAGCATGCCAA	1560
QY	1573	GCTCTCGCTGACGAGCTGACGTGGAAGATGAGCGTGGGACACGCTTGGCTGGCGAG	1632
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QY	1753	TGTACGAGAGACCGTTTCAAAGAACACAGGCTCTTTTTCACCGGAAGTGTGTGAG	1812
DB	1741	TGTACGAGAGACCGTTTCAAAGAACACAGGCTCTTTTTCACCGGAAGTGTGTGAG	1800
QY	1813	CAAGTTGCAAGACTTGAATCAGACACACTTGAAGAGGTGACGTCGCGGAGCTGTC	1872
DB	1801	CAAGTTGCAAGACTTGAATCAGACACACTTGAAGAGGTGACGTCGCGGAGCTGTC	1860
QY	1873	GGAACAGAGTTCAGGACAGCATCGGGAAGCCAGGCGCCCTGCTGACGTCCAGACTCGG	1932
DB	1861	GGAACAGAGTTCAGGACAGCATCGGGAAGCCAGGCGCCCTGCTGACGTCCAGACTCGG	1920
QY	1933	CTTCATCCCAAGCTGACGGCTGCGGCGGATGTGAACATGACACTACGTCGTGGGAGC	1992
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QY	1993	CAGAACGTTCCGACAGAAAGAGGCGGAGCGTCTACCTCGAGGTTGAAGGCACTGTT	2052
DB	1981	CAGAACGTTCCGACAGAAAGAGGCGGAGCGTCTACCTCGAGGTTGAAGGCACTGTT	2040
QY	2053	CAGCGTGTCAACTACGAGCGGCGGCGGCCCTGCTGGCGCTCTGTGCTGGG	2112
DB	2041	CAGCGTGTCAACTACGAGCGGCGGCGGCCCTGCTGGCGCTCTGTGCTGGG	2100
QY	2113	CCTGGACGATATCCACAGGCTGCGCGACCTTCGTGCTGCTGTGGGGCCACGAGACC	2172
DB	2101	CCTGGACGATATCCACAGGCTGCGCGACCTTCGTGCTGCTGTGGGGCCACGAGACC	2160
QY	2173	GCCGCTGAGCTGTACTTGTCAAGGTGGATGTGACGGGCGGTACGACACATCCCCCA	2232
DB	2161	GCCGCTGAGCTGTACTTGTCAAGGTGGATGTGACGGGCGGTACGACACATCCCCCA	2220
QY	2233	GGACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGACACGTACTGCTGGG	2292
DB	2221	GGACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGACACGTACTGCTGGG	2280
QY	2293	TCGGTATGCCGTGTCCAGAGGCGGCCATGCGGACGTCGCGAAGGCTTCAAGAGCCA	2352
DB	2281	TCGGTATGCCGTGTCCAGAGGCGGCCATGCGGACGTCGCGAAGGCTTCAAGAGCCA	2340

QY	2353	CGTCTCTACTTGACAGACCTCCAGCGGTACATGCGAGTTCTGGTCACTCGAGGA	2412
DB	2341	CGTCTCTACTTGACAGACCTCCAGCGGTACATGCGAGTTCTGGTCACTCGAGGA	2400
QY	2413	GACCAACCCCGTGGAGGATGCGGTGTCATCAGCAGAGCTCCTCCCTGAATGAGGCCAG	2472
DB	2401	GACCAACCCCGTGGAGGATGCGGTGTCATCAGCAGAGCTCCTCCCTGAATGAGGCCAG	2460
QY	2473	GAGTGGCTCTTCGAGCTCTTCCATAGGTTCATGTGCCACACGCGTGCATCAGGGG	2532
DB	2461	CAGTGGCTCTTCGAGCTCTTCCATAGGTTCATGTGCCACACGCGTGCATCAGGGG	2520
QY	2533	CAAGTCTCAGTCCAGTCCAGGGATCCGCGAGGCTCCATCCTCTCCACGCTGCTCTG	2592
DB	2521	CAAGTCTCAGTCCAGTCCAGGGATCCGCGAGGCTCCATCCTCTCCACGCTGCTCTG	2580
QY	2593	CAGCCTGTGCTACGCGGACATGGAGAACAGCTGTTGGGGGATTCGGCGGAGCGGCT	2652
DB	2581	CAGCCTGTGCTACGCGGACATGGAGAACAGCTGTTGGGGGATTCGGCGGAGCGGCT	2640
QY	2653	GCTCTCGGTTTGGTGGATGATTTCTTGTGTGACACCTCACCACCGCGAAAC	2712
DB	2641	GCTCTCGGTTTGGTGGATGATTTCTTGTGTGACACCTCACCACCGCGAAAC	2700
QY	2713	CTTCTCAGGACCCCTGGTCCGAGGTGCTCCCTGAGTATGGCTGGTGAACCTTGGGNA	2772
DB	2701	CTTCTCAGGACCCCTGGTCCGAGGTGCTCCCTGAGTATGGCTGGTGAACCTTGGGNA	2760
QY	2773	GACAGTGTGAACCTTCCCTGTAGAAAGAGAGGCGCTGGTGCGACGGCTTTTGTTCAGAT	2832
DB	2761	GACAGTGTGAACCTTCCCTGTAGAAAGAGAGGCGCTGGTGCGACGGCTTTTGTTCAGAT	2820
QY	2833	GCGGCGCACGGCTTATCCCTGTGTGGGCTGCTGTGTGATACCCGACCCCTGGAGT	2892
DB	2821	GCGGCGCACGGCTTATCCCTGTGTGGGCTGCTGTGTGATACCCGACCCCTGGAGT	2880
QY	2893	GCAGAGGCACTACTCCAGCTATGCCGCGACCTCCATCAGAGCCAGTCTCACCTTCAACGG	2952
DB	2881	GCAGAGGCACTACTCCAGCTATGCCGCGACCTCCATCAGAGCCAGTCTCACCTTCAACGG	2940
QY	2953	GCGCTTCAAGGCTGGGAGAACATCGTTCGCAAACTCTTTGGGGTCTTGGGCTCAAGTG	3012
DB	2941	GCGCTTCAAGGCTGGGAGAACATCGTTCGCAAACTCTTTGGGGTCTTGGGCTCAAGTG	3000
QY	3013	TCACAGCTGTTCCTGAGTTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA	3072
DB	3001	TCACAGCTGTTCCTGAGTTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA	3060
QY	3073	CAAGATCTCTGCTGCGAGGCTACAGGTTTACGCGATGTGTGCTGAGCTCCCATTTCA	3132
DB	3061	CAAGATCTCTGCTGCGAGGCTACAGGTTTACGCGATGTGTGCTGAGCTCCCATTTCA	3120
QY	3133	TCAGCAAGTTTGGAAAGAACCCACATTTTTCCTGCGCGCTCATCTGTGACAGCGCTCCCT	3192
DB	3121	TCAGCAAGTTTGGAAAGAACCCACATTTTTCCTGCGCGCTCATCTGTGACAGCGCTCCCT	3180
QY	3193	CTGCTACTCCATTCCTGAAAGCAAGAACGAGGATGTGCTGGGGGCAAGGGCGCGCG	3252
DB	3181	CTGCTACTCCATTCCTGAAAGCAAGAACGAGGATGTGCTGGGGGCAAGGGCGCGCG	3240
QY	3253	GCGGCTCTGCGCTCCGAGGCGGTGCGTGGTGTGCCAACCAAGATTCCTGCTCAAGCT	3312
DB	3241	GCGGCTCTGCGCTCCGAGGCGGTGCGTGGTGTGCCAACCAAGATTCCTGCTCAAGCT	3300
QY	3313	GACTCGACACGCTGTCACCTAGTGCCACTCTGCGGGTCACTCAGGAGCGCCACACCA	3372
DB	3301	GACTCGACACGCTGTCACCTAGTGCCACTCTGCGGGTCACTCAGGAGCGCCACACCA	3360
QY	3373	GCTGAGTCGGAAGCTCCCGGGGACACGCTGACTGCTGAGGCGCGGACCAACCCCGC	3432
DB	3361	GCTGAGTCGGAAGCTCCCGGGGACACGCTGACTGCTGAGGCGCGGACCAACCCCGC	3420
QY	3433	ACTGCGCTCAGACTTCAAGACCATCCTGGACTGTGTCGACCCGCCACAGCCAGCGGA	3492



Db 3421 ACTGCCCTCAGACTTCAGACCACTCTGACTGATGGCCACCCGCCACAGCCAGGCCGA 3480  
QY 3493 GAGCAGACACCAAGCCCTGTACACCCCGGGCTCTACGTCCTCCAGGAGGAGGGGGGCC 3552  
Db 3481 GAGCAGACACCAAGCCCTGTACACCCCGGGCTCTACGTCCTCCAGGAGGAGGGGGGCC 3540  
QY 3553 CACACCCAGCCCGCAGCCGTGGAGTCTGAGGCCCTGAGTGTGTTGGCCGAGGCCCTG 3612  
Db 3541 CACACCCAGCCCGCAGCCGTGGAGTCTGAGGCCCTGAGTGTGTTGGCCGAGGCCCTG 3600  
QY 3613 CATGTCCGGCTGAAGCTGAGTGTCCGGCTGAGGCCCTGAGGCCCTGAGGCCCTGAGGCCCTG 3672  
Db 3601 CATGTCCGGCTGAAGCTGAGTGTCCGGCTGAGGCCCTGAGGCCCTGAGGCCCTGAGGCCCTG 3660  
QY 3673 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA 3732  
Db 3661 GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA 3720  
QY 3733 GGCCAGCTTTCTCCACAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3792  
Db 3721 GGCCAGCTTTCTCCACAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780  
QY 3793 CCTGAT 3798  
Db 3781 CCAGAT 3786

RESULT 5

US-10-053-758-224  
; Sequence 224, Application US/10053758  
; Publication No. US20030032075A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. US20030032075A1el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/053,758  
; FILING DATE: 18-Jan-2002  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 224:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4015 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 56..3454  
; OTHER INFORMATION: /product= "htrr"  
; /note= "human telomerase reverse  
; transcriptase (htrr) catalytic protein  
; component"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 224:  
; US-10-053-758-224  
Query Match 99.6%; Score 3784.4; DB 14; Length 4015;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 13 GCAGCGTGGCTGCTGCGACAGTGGGAGCCCTGGCCCCCGGACACCCCGGATGCC 72  
Db 1 GCAGCGTGGCTGCTGCGACAGTGGGAGCCCTGGCCCCCGGATGCC 60  
QY 73 GCGCGTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCAGCAGCTACCGCGAGTGC 132  
Db 61 GCGCGTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCAGCAGCTACCGCGAGTGC 120  
QY 133 GCGCGTGGCCACATTTGCTGCGGCGCCTTGGGGCCCCCAGGGCTGGCGGTGGTGCAGCGCG 192  
Db 121 GCGCGTGGCCACATTTGCTGCGGCGCCTTGGGGCCCCCAGGGCTGGCGGTGGTGCAGCGCG 180  
QY 193 GGACCGGGGGCTTTCCGGCGCTGGTGGCCCCAGTGGCTGGTGGTGGTGGTGGTGGTGG 252  
Db 181 GGACCGGGGGCTTTCCGGCGCTGGTGGCCCCAGTGGCTGGTGGTGGTGGTGGTGGTGG 240  
QY 253 ACGGCGCCCCCGCGCGCCCTTCCCTCCCGCAGGTGCTGCTGCTGAAGAGTGGTGGC 312  
Db 241 ACGGCGCCCCCGCGCGCCCTTCCCTCCCGCAGGTGCTGCTGCTGAAGAGTGGTGGC 300  
QY 313 CCGAGTGTCTGACAGAGTGTGCGAGCGCGCGCGAAGAACGCTGCTGGCTTCGGCTTCGC 372  
Db 301 CCGAGTGTCTGACAGAGTGTGCGAGCGCGCGCGAAGAACGCTGCTGGCTTCGC 360  
QY 373 GCTGCTGGAGGGGGCGGG 432  
Db 361 GCTGCTGGAGGG 420  
QY 433 CTTGCCCAACACAGCTGACCGACACTTGGGGGGAGGGGGGGGGGGGGGGGGGGGGGGGG 492  
Db 421 CTTGCCCAACACAGCTGACCGACACTTGGGGGGAGGGGGGGGGGGGGGGGGGGGGGGGG 480  
QY 493 CCGCGTGGCGAGCAGTGTGTTCACTTGTGTCACCTGCTGGCACGCTGGCGCTTTTGTGTGT 552  
Db 481 CCGCGTGGCGAGCAGTGTGTTCACTTGTGTTCACTTGTGTCACCTGCTGGCACGCTTTTGTGTGT 540  
QY 553 GGCTCCAGCTGGCCCTACCAAGTGTGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 612  
Db 541 GGCTCCAGCTGGCCCTACCAAGTGTGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 600  
QY 613 TCAGGGCGGG 672  
Db 601 TCAGGGCGGG 660  
QY 673 CTGGAACCATAGCGTTCAGGGAGCCCGGGTCCCGCTGGGGCTCCAGACCCCGGGTGGCAG 732  
Db 661 CTGGAACCATAGCGTTCAGGGAGCCCGGGTCCCGCTGGGGCTCCAGACCCCGGGTGGCAG 720  
QY 733 GAGGCGGGGGGGGAGTGCACCGCCAGAGTCTGCGTTGCCCCAAGAGGGGGGAGGCGTGGCGC 792







Db	721	GAGGCGGGGCGAGTCCAGCCGAAGTCTGCCGTTGCCAAGAGAGCCCGAGCGGTGGCG	780
QY	793	TGCCCCGTAGCCGGAGCGACCCCGTGGGACAGGGTCTTGCGGCCACCCCGGGCAGGAC	852
Db	781	TGCCCCGTAGCCGGAGCGACCCCGTGGGACAGGGTCTTGCGGCCACCCCGGGCAGGAC	840
QY	853	GGGTGACCGAGTACCGGTGGTTCTGTGTGGTGTCACTGCGCAGACCCGCGAAGAAGC	912
Db	841	GGGTGACCGAGTACCGGTGGTTCTGTGTGGTGTCACTGCGCAGACCCGCGAAGAAGC	900
QY	913	CACCTTTTGGAGGTGGCTCTCTGGACGCGCCACTGCCATCCACCCTCGTGGGCGGCA	972
Db	901	CACCTTTTGGAGGTGGCTCTCTGGACGCGCCACTGCCATCCACCCTCGTGGGCGGCA	960
QY	973	GCACACGGGGCGCCCGCATCCACATCGGGGCCACCGTCCCTGGGACACGCTTGTC	1032
Db	961	GCACACGGGGCGCCCGCATCCACATCGGGGCCACCGTCCCTGGGACACGCTTGTC	1020
QY	1033	CCCGGTGACGCCGAGACCAAGCACTTCCTCTACTCTCAGCGCACAGGAGCAGCTGG	1092
Db	1021	CCCGGTGACGCCGAGACCAAGCACTTCCTCTACTCTCAGCGCACAGGAGCAGCTGG	1080
QY	1093	GGCCTCTCTTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGTCTGGAGGCTCGTGA	1152
Db	1081	GGCCTCTCTTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGTCTGGAGGCTCGTGA	1140
QY	1153	GACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCGCGT	1212
Db	1141	GACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCGCGT	1200
QY	1213	GCCCCAGCGCTACTGGCAAAATCGGCCCTGTTCTGGAGTGTCTTGGAAACACCGCA	1272
Db	1201	GCCCCAGCGCTACTGGCAAAATCGGCCCTGTTCTGGAGTGTCTTGGAAACACCGCA	1260
QY	1273	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTCGAGCTGCGGTCACCCAGC	1332
Db	1261	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTCGAGCTGCGGTCACCCAGC	1320
QY	1333	AGCCGGTGTCTGTCGCCGGGAGAACGCCAGGGCTCTGTGGGGCGCCCGAGGAGGGA	1392
Db	1321	AGCCGGTGTCTGTCGCCGGGAGAACGCCAGGGCTCTGTGGGGCGCCCGAGGAGGGA	1380
QY	1393	CACAGACCCCGTGCCTGGTGCAGTGCCTCGCCGACGACAGCAGCCCTGGCAGGTGA	1452
Db	1381	CACAGACCCCGTGCCTGGTGCAGTGCCTCGCCGACGACAGCAGCCCTGGCAGGTGA	1440
QY	1453	CGGCTTCGTGGGGCTGCCTCGCCGGGTGTGCCCGCAGCCCTGCGGGTCCAGGCA	1512
Db	1441	CGGCTTCGTGGGGCTGCCTCGCCGGGTGTGCCCGCAGCCCTGCGGGTCCAGGCA	1500
QY	1513	CAACGAACCCCGTTCCTCAGGAACACCAAGTTTCATCTCCCTGGGGAAGCATGCCAA	1572
Db	1501	CAACGAACCCCGTTCCTCAGGAACACCAAGTTTCATCTCCCTGGGGAAGCATGCCAA	1560
QY	1573	GCTCTCGTGCAGGAGTACGTGTGAGATGAGCGTGGGGACTGGCTTGGCTGGCAG	1632
Db	1561	GCTCTCGTGCAGGAGTACGTGTGAGATGAGCGTGGGGACTGGCTTGGCTGGCAG	1620
QY	1633	GAGCCACAGGGTGGCTGTGTTCGCGCCGACAGACACCGTCTGCGTGGAGAGATCCTGGC	1692
Db	1621	GAGCCACAGGGTGGCTGTGTTCGCGCCGACAGACACCGTCTGCGTGGAGAGATCCTGGC	1680
QY	1693	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCTCGAGCTGCTCAGGTCTTTCTTTTA	1752
Db	1681	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCTCGAGCTGCTCAGGTCTTTCTTTTA	1740
QY	1753	TGTCAGGAGACCGTTTCAAAGAACAGGCTCTTTTCTACCGGAGAGTGTCTGGAG	1812
Db	1741	TGTCAGGAGACCGTTTCAAAGAACAGGCTCTTTTCTACCGGAGAGTGTCTGGAG	1800
QY	1813	CAAGTTGAAAGCATTTGGAATCAGACACACTTGAAGGGGTGACGCTCGGGAGCTGTC	1872
Db	1801	CAAGTTGAAAGCATTTGGAATCAGACACACTTGAAGGGGTGACGCTCGGGAGCTGTC	1860
QY	1873	GGAAAGCAGAGGTACGGCAGCATCGGAAAGCCAGGCCCGCCCTGCTGACGCTCCAGACTCG	1932
Db	1861	GGAAAGCAGAGGTACGGCAGCATCGGAAAGCCAGGCCCGCCCTGCTGACGCTCCAGACTCG	1920
QY	1933	CTTTCATCCCAAGCCTGACGGCTGCGGCCGATTGTGAACATGGACTAGCTGCTGGGAGC	1992
Db	1921	CTTTCATCCCAAGCCTGACGGCTGCGGCCGATTGTGAACATGGACTAGCTGCTGGGAGC	1980
QY	1993	CAGAACTTCCGAGAGAAAGAGGCCGAGCGTCTACCTCGAGGGTGAAGCACTGTT	2052
Db	1981	CAGAACTTCCGAGAGAAAGAGGCCGAGCGTCTACCTCGAGGGTGAAGCACTGTT	2040
QY	2053	CAGCGTGTCAACTAGCAGCGGGCGGCCGCCCGCCCTCTCTGGGGCGCTCTGTGTGGG	2112
Db	2041	CAGCGTGTCAACTAGCAGCGGGCGGCCGCCCGCCCTCTCTGGGGCGCTCTGTGTGGG	2100
QY	2113	CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGTGCGGGCCACAGACCC	2172
Db	2101	CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGTGCGGGCCACAGACCC	2160
QY	2173	GCCGCTGAGCTGTACTTTTCAAGGTGATGTGAGGGCGGCTACGACACCATCCCCCA	2232
Db	2161	GCCGCTGAGCTGTACTTTTCAAGGTGATGTGAGGGCGGCTACGACACCATCCCCCA	2220
QY	2233	GGACAGGCTACGGAGGTTCATGCCAGCATCATCAAAACCCACAGACACGCTACTGCTGG	2292
Db	2221	GGACAGGCTACGGAGGTTCATGCCAGCATCATCAAAACCCACAGACACGCTACTGCTGG	2280
QY	2293	TGCGTATGCGGTGGTCCAGAAGCCGCCCATGGGCACGTCGCGAAGGCTTCAAGAGCCA	2352
Db	2281	TGCGTATGCGGTGGTCCAGAAGCCGCCCATGGGCACGTCGCGAAGGCTTCAAGAGCCA	2340
QY	2353	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCCTGACGA	2412
Db	2341	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCCTGACGA	2400
QY	2413	GACCAGCCGCTGAGGGATGCCGTGTCATCAGCAGAGAGCTCCTCCTCAATGAGGCCAG	2472
Db	2401	GACCAGCCGCTGAGGGATGCCGTGTCATCAGCAGAGAGCTCCTCCTCAATGAGGCCAG	2460
QY	2473	CAGTGGCTCTTCGAGCTCTTCTACGCTTCATGTGCCACACGCGCTGCGCATCAGGGG	2532
Db	2461	CAGTGGCTCTTCGAGCTCTTCTACGCTTCATGTGCCACACGCGCTGCGCATCAGGGG	2520
QY	2533	CAAGTCTACGTCCAGTGCCAGGGATCCCGAGGGCTCCATCCTCTCCACGCTGCTCTG	2592
Db	2521	CAAGTCTACGTCCAGTGCCAGGGATCCCGAGGGCTCCATCCTCTCCACGCTGCTCTG	2580
QY	2593	CAGCCTGTGCTACGGGGACATGGAGAACAAAGCTGTTGGGGGATTCGGGGGACGGCT	2652
Db	2581	CAGCCTGTGCTACGGGGACATGGAGAACAAAGCTGTTGGGGGATTCGGGGGACGGCT	2640
QY	2653	GCTCTGCTGCTTGGTGGATTTCTTGTGTGACACCTCACCCTCACCACCGCGAAAC	2712
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QY	2713	CTTCTCAGAACCCCTGCTCCGAGGTCTCCTCAGATGCTGCTGCTGCTGCTGCTGCTG	2772
Db	2701	CTTCTCAGAACCCCTGCTCCGAGGTCTCCTCAGATGCTGCTGCTGCTGCTGCTGCTG	2760
QY	2773	GACAGTGTGAATCTCCCTGTAGAAAGACAGGCCCTGGGTGGACAGGCTTTTGTTCAGAT	2832
Db	2761	GACAGTGTGAATCTCCCTGTAGAAAGACAGGCCCTGGGTGGACAGGCTTTTGTTCAGAT	2820
QY	2833	GCCGGCCACGGCCTATTCCTCTGCTGGCGCTGCTGCTGATACCCGACCCCTGGAGGT	2892
Db	2821	GCCGGCCACGGCCTATTCCTCTGCTGGCGCTGCTGCTGATACCCGACCCCTGGAGGT	2880
QY	2893	GCAGAGCAGCTACTCCAGCTATGCCGGACCTCCATCAGAGCAGCTCCTCACCCTTCAACCG	2952
Db	2881	GCAGAGCAGCTACTCCAGCTATGCCGGACCTCCATCAGAGCAGCTCCTCACCCTTCAACCG	2940

QY 2953 CGGCTTCAAGCTGGGAGAACATGCTCGAATACTCTTTGGGGTCTTTGGGGTGAAGTG 3012  
Db 2941 CGGCTTCAAGCTGGGAGAACATGCTCGAATACTCTTTGGGGTCTTTGGGGTGAAGTG 3000  
QY 3013 TCACAGCTGTCTTGTGATTTGACAGTGAACAGCTCCAGACGCTGTGCACCAACATCTA 3072  
Db 3001 TCACAGCTGTCTTGTGATTTGACAGTGAACAGCTCCAGACGCTGTGCACCAACATCTA 3060  
QY 3073 CAAGATCCTCTGCTGACGAGCTACAGTGTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3132  
Db 3061 CAAGATCCTCTGCTGACGAGCTACAGTGTTCACGCATGTGTGCTGCAGCTCCCATTTCA 3120  
QY 3133 TCAGCAAGTTTGAAGAACCCACATTTTCTTGGGGTCTATCTGTACACGCGCTCCCT 3192  
Db 3121 TCAGCAAGTTTGAAGAACCCACATTTTCTTGGGGTCTATCTGTACACGCGCTCCCT 3180  
QY 3193 CTGCTACTCATCTGTAAGCCAGACGAGGATGTCTGCTGGGGCCCAAGGCGCGC 3252  
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QY 3253 CGGCTCTCTGCTCCGAGGCGGTGACGTGGCTGTGCCACCAAGCATTTCTGTCAAGCT 3312  
Db 3241 CGGCTCTCTGCTCCGAGGCGGTGACGTGGCTGTGCCACCAAGCATTTCTGTCAAGCT 3300  
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QY 3373 GCTGAGTCGGAAGCTCCCGGGAGGAGCTGACTGCTGAGGCGCCAGGCGCCAGCCGCG 3432  
Db 3361 GCTGAGTCGGAAGCTCCCGGGAGGAGCTGACTGCTGAGGCGCCAGGCGCCAGCCGCG 3420  
QY 3433 ACTGCTCTCAGACTTCAAGACCATCTCTGGACTGATGGCCACCGCCACAGCCAGGCGCGA 3492  
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RESULT 7  
US-10-054-295-224  
; Sequence 224, Application US/10054295  
; Publication No. US20030044953A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.

; TITLE OF INVENTION: No. US20030044953A1el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/054,295  
; FILING DATE: 18-Jan-2002  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/854,050  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 224:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4015 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 56..3454  
; OTHER INFORMATION: /product= "hTERT"  
; /note= "human telomerase reverse  
; transcriptase (hTERT) catalytic protein  
; component"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 224:  
US-10-054-295-224

Query Match 99.68; Score 3784.4; DB 14; Length 4015;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 13 GCAGCGCTCGCTCTGCTGCGACGTGGGAGCCCTGCCCGCCACCCCGCGATGCC 72  
Db 1 GCAGCGCTCGCTCTGCTGCGACGTGGGAGCCCTGCCCGCCACCCCGCGATGCC 60  
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QY 133 GCGCGTGGCCACGTTCGTGCGGCGCTTGGGGCCCGAGGCTGGCGGCTGTGTCAGCGCGG 192  
Db 121 GCGCGTGGCCACGTTCGTGCGGCGCTTGGGGCCCGAGGCTGGCGGCTGTGTCAGCGCGG 180  
QY 193 GGACCCGCGCGCTTTCCGCGCGCTGTGTGCCAGTGTGCTGCTGCGCAGCCACTACCGCGAGCGC 252  
Db 181 GGACCCGCGCGCTTTCCGCGCGCTGTGTGCCAGTGTGCTGCTGCGCAGCGCTGTGCTGGGAGCG 240  
QY 253 ACGGCGCGCCCGCGCGCCCGCTTCCCTCCCGCCAGGCTGTCTGCTGAAGGAGCTGTGGG 312

Db	241	ACGGCCGCCCGCCGCCCGCCCTCTCTCCGACAGGTGTCTCGCTGAAGGAGCTGTGTC	300
QY	313	CCGAGTGTCTGCAGAGCTGTGCGAGCGCGGGCGGAAGACGTGCTGGCCCTTGGGCTTCGC	372
Db	301	CCGAGTGTCTGCAGAGCTGTGCGAGCGCGGGCGGAAGACGTGCTGGCCCTTGGGCTTCGC	360
QY	373	GCTGCTGGACGGGGCCCGGGGGCCCGCCCGGAGGCGCTTACACACAGAGGTGCGCAGCTA	432
Db	361	GCTGCTGGACGGGGCCCGGGGGCCCGCCCGGAGGCGCTTACACACAGAGGTGCGCAGCTA	420
QY	433	CTTGCCCAACACGGTGACCGACGCTGCGGGGGAGCGGGGGCTGCTGCTGTCG	492
Db	421	CTTGCCCAACACGGTGACCGACGCTGCGGGGGAGCGGGGGCTGCTGCTGTCG	480
QY	493	CCGCGTGGCGAGCAGCTGCTGGTTACCTGCTGGACGCTCGCGGCTCTTTGTGTGCT	552
Db	481	CCGCGTGGCGAGCAGCTGCTGGTTACCTGCTGGACGCTCGCGGCTCTTTGTGTGCT	540
QY	553	GGCTCCAGCTGCGGCTACAGGTGTGCGGGCGCGGCTGTACACGCTCGGGCTGCCAC	612
Db	541	GGCTCCAGCTGCGGCTACAGGTGTGCGGGCGCGGCTGTACACGCTCGGGCTGCCAC	600
QY	613	TCAGGCCCGCCCGCCACACGCTAGTGGACCCCGAAGCGCTCTGGGATGCGAAGCGGC	672
Db	601	TCAGGCCCGCCCGCCACACGCTAGTGGACCCCGAAGCGCTCTGGGATGCGAAGCGGC	660
QY	673	CTGGAAACCATAGGCTCAGGAGCGCGGGGTCCCGCTGGGCTGCCAGCCCGGGTGGAG	732
Db	661	CTGGAAACCATAGGCTCAGGAGCGCGGGGTCCCGCTGGGCTGCCAGCCCGGGTGGAG	720
QY	733	GAGGCGGGGCGAGTGCACGCGGAAGTCTGCGGTTGCCAAGAGGCCAGGGCGTGGCGC	792
Db	721	GAGGCGGGGCGAGTGCACGCGGAAGTCTGCGGTTGCCAAGAGGCCAGGGCGTGGCGC	780
QY	793	TGCCCCTAGCCGGAGCGAGCGCCCGTTGGGACAGGGGTCTTGCGGCCACCCCGGGCAGGAC	852
Db	781	TGCCCCTAGCCGGAGCGAGCGCCCGTTGGGACAGGGGTCTTGCGGCCACCCCGGGCAGGAC	840
QY	853	GGTGGACCGAGTGACCGTGGTTCTGTGTGTGTGTACCTGCCAGACCCCGCGAAGAC	912
Db	841	GGTGGACCGAGTGACCGTGGTTCTGTGTGTGTGTACCTGCCAGACCCCGCGAAGAC	900
QY	913	CACCTCTTTGGAGGTGCGCTCTCTGGCACGGGCCACTCCACCATCCGTGGGCCGCCA	972
Db	901	CACCTCTTTGGAGGTGCGCTCTCTGGCACGGGCCACTCCACCATCCGTGGGCCGCCA	960
QY	973	GCACACGGGGCCCCCATTCACATPCACATPCGCGGCCACACGTCTCGTGGACACGCTTGTCC	1032
Db	961	GCACACGGGGCCCCCATTCACATPCGCGGCCACACGTCTCGTGGACACGCTTGTCC	1020
QY	1033	CCGGGTGTACGGGAGACCAAGCACTTCTCTACTCTCCTCAGGCGCAAGGACGAGTGGC	1092
Db	1021	CCGGGTGTACGGGAGACCAAGCACTTCTCTACTCTCCTCAGGCGCAAGGACGAGTGGC	1080
QY	1093	GCCCTCTTCTTACTCAGCTCTCTGAGGCCACGCTGACTTGGCGCTTCGGAGGCTCGTGA	1152
Db	1081	GCCCTCTTCTTACTCAGCTCTCTGAGGCCACGCTGACTTGGCGCTCGGAGGCTCGTGA	1140
QY	1153	GACCAFTCTTCTGCGGTTCACGCGCTTGGATGCCAGGACTTCCCGCAGGTTGCCCGGCT	1212
Db	1141	GACCAFTCTTCTGCGGTTCACGCGCTTGGATGCCAGGACTTCCCGCAGGTTGCCCGGCT	1200
QY	1213	GCCCCAGCGCTACTGGCAATGGGCCCCGTGTTCTGGAGCTGCTTGGGAACCAACGCGCA	1272
Db	1201	GCCCCAGCGCTACTGGCAATGGGCCCCGTGTTCTGGAGCTGCTTGGGAACCAACGCGCA	1260
QY	1273	GTGCCCTTACGGGGTCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCACG	1332
Db	1261	GTGCCCTTACGGGGTCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCACG	1320
QY	1333	AGCCGGTGTCTGTGCCCGGAGAACCCCGAGGGCTCTGTGGCGGCCCGCCGAGGAGGA	1392
Db	1321	AGCCGGTGTCTGTGCCCGGAGAACCCCGAGGGCTCTGTGGCGGCCCGCCGAGGAGGA	1380
QY	1393	CACAGACCCCCGCTCGCCTGGTGCAGCTGCTCCGCCACACAGAGACCCCTTGGCAGGTGA	1452
Db	1381	CACAGACCCCCGCTCGCCTGGTGCAGCTGCTCCGCCACACAGAGACCCCTTGGCAGGTGA	1440
QY	1453	CGGCTTCTGTGGGGGCTGCTGCGCGGCTGTGTGCCCGCCAGGCTCTGGGGCTTCCAGGCA	1512
Db	1441	CGGCTTCTGTGGGGGCTGCTGCGCGGCTGTGTGCCCGCCAGGCTCTGGGGCTTCCAGGCA	1500
QY	1513	CAACGAACGCCGCTTCTCCTCAGGAACACCAAGAGTTTATCTCCTCGGGGAAGCATGCCAA	1572
Db	1501	CAACGAACGCCGCTTCTCCTCAGGAACACCAAGAGTTTATCTCCTCGGGGAAGCATGCCAA	1560
QY	1573	GCTCTCGCTGCAGGAGCTGACGTGGAAGATGACGTGCGGGACTGCGCTTGGCTGGCCAG	1632
Db	1561	GCTCTCGCTGCAGGAGCTGACGTGGAAGATGACGTGCGGGACTGCGCTTGGCTGGCCAG	1620
QY	1633	GAGCCAGGGGTGGGCTGTTCGGCGCCAGACACCGTCTCGCTGAGGAGATCTCTGGC	1692
Db	1621	GAGCCAGGGGTGGGCTGTTCGGCGCCAGACACCGTCTCGCTGAGGAGATCTCTGGC	1680
QY	1693	CAAGTTCCTGCACTGCTGATGATGTGTACGTCTGTCGAGCTGCTCAGGCTCTTTT	1752
Db	1681	CAAGTTCCTGCACTGCTGATGATGTGTACGTCTGTCGAGCTGCTCAGGCTCTTTT	1740
QY	1753	TGTCACGGAGACCCACCTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTCTCTGGAG	1812
Db	1741	TGTCACGGAGACCCACCTTTCAAAGAACAGGCTCTTTTCTACCGGAAGAGTCTCTGGAG	1800
QY	1813	CAAGTTGCAAGCATTTGGAATCAGACAGACACTTGAAGAGGGTGCAGCTGGCGGAGCTGTC	1872
Db	1801	CAAGTTGCAAGCATTTGGAATCAGACAGACACTTGAAGAGGGTGCAGCTGGCGGAGCTGTC	1860
QY	1873	GGAGCAGAGGTTCAGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCACAGCTCG	1932
Db	1861	GGAGCAGAGGTTCAGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCACAGCTCG	1920
QY	1933	CTTCTATCCCAAGCCTGACGGGTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGGAGC	1992
Db	1921	CTTCTATCCCAAGCCTGACGGGTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGGAGC	1980
QY	1993	CAGACGTTTCCCGCAGAAAGAGGCGCGAGCGCTCTCACCTCAGAGGGTGAAGCACTGTT	2052
Db	1981	CAGACGTTTCCCGCAGAAAGAGGCGCGAGCGCTCTCACCTCAGAGGGTGAAGCACTGTT	2040
QY	2053	CAGCGTGTCTAACTACAGGGGCGCGGCGCCCGCGCTCTCTGGGCGCTCTGTGTGGG	2112
Db	2041	CAGCGTGTCTAACTACAGGGGCGCGGCGCCCGCGCTCTCTGGGCGCTCTGTGTGGG	2100
QY	2113	CTTGGACGATATCCACAGGSCCTGGCGCACCTTCTGCTGCTGCTGGGCGCCAGGACCC	2172
Db	2101	CTTGGACGATATCCACAGGSCCTGGCGCACCTTCTGCTGCTGCTGGGCGCCAGGACCC	2160
QY	2173	GCGGCTTCTGAGCTTCTCAAGGTGGATGTGAGGGGCGCTAGCACACCATCCCGCA	2232
Db	2161	GCGGCTTCTGAGCTTCTCAAGGTGGATGTGAGGGGCGCTAGCACACCATCCCGCA	2220
QY	2233	GGACAGGCTCAGGAGGTCTATCGCCAGCATCATCAAACCCAGAACACAGTACTGCTGGC	2292
Db	2221	GGACAGGCTCAGGAGGTCTATCGCCAGCATCATCAAACCCAGAACACAGTACTGCTGGC	2280
QY	2293	TGCGTATGCGGTGCTCCAGAGGCCCGCCATGGGACGTCGCCGAGGCTTCAAGAGCCA	2352
Db	2281	TGCGTATGCGGTGCTCCAGAGGCCCGCCATGGGACGTCGCCGAGGCTTCAAGAGCCA	2340
QY	2353	CGTCTTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGGCTCACCTGAGGA	2412
Db	2341	CGTCTTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGGCTCACCTGAGGA	2400
QY	2413	GACCAAGCCGCTGAGGATGCGCTGCTCATGAGCAGAGCTCTCCCTGAATGAGGCCAG	2472
Db	2401	GACCAAGCCGCTGAGGATGCGCTGCTCATGAGCAGAGCTCTCCCTGAATGAGGCCAG	2460

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Db 2461 CAGTGGCTCTTCGACGCTCTTCTACGCTTCATGTGCGCACACGCGCTGCGCATCAGGG 2520  
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QY 2773 GACAGTGGTGAACCTCCCTTAGAAGACGAGGGCCCTGGGTGGACGGCTTTTGTTCAGAT 2832  
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QY 3133 TCAGCAAGTTTGAAGAACCCACATTTTCTCGCGTCACTCTGACACGGCTCCCT 3192  
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Db 3121 TCAGCAAGTTTGAAGAACCCACATTTTCTCGCGTCACTCTGACACGGCTCCCT 3180  
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Db 3181 CTGCTACTCATCTGAAAGCCAAAGACGAGGATGTGCTGGGGCCCAAGGGCGCGC 3240  
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Db 3241 CGGCGCTCTGCCCTCCGAGGCGCTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300  
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Db 3301 GACTCGACACCGTGTCACTTACCTTACCTTCCCTGCGGTCACTCAGGACAGCCAGAGCCA 3360  
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Db 3361 GCTGAGTCGAAGCTCCCGGGAGAGAGCTGACTGCTGGAGCGCGCAGCCAGCGCGC 3420  
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|||||  
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTTGGACTGATGGCCACCCGCGCAGCCAGCGCGC 3480  
|||||  
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|||||  
Db 3481 GAGCAGACACAGAGCCCTGTTCACGCCGGCTCTACGTCCCGAGGAGGAGGGCGGCC 3540  
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QY 3553 CACACCGAGCCCGCACCGCTGGGAGTCTGAGGCTGAGTGTGTTGGCCGAGGCGCTG 3612  
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Db 3541 CACACCCAGGCCCGCACCGCTGGAGTCTGAGGCTGAGTGTGTTGGCCGAGGCGCTG 3600  
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QY 3613 CATGTCGGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGAGTGTCCAGCCAAAGGCT 3672  
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Db 3601 CATGTCGGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGAGTGTCCAGCCAAAGGCT 3660  
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QY 3673 GAGTGTCCAGCACACCTGCGCTTCTACTTCCCCACAGGCTGCGGCTCCACCCCA 3732  
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Db 3661 GAGTGTCCAGCACACCTGCGCTTCTACTTCCCCACAGGCTGCGGCTCCACCCCA 3720  
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QY 3733 GGGCCAGCTTTTCTCACCAGGCGCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3792  
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Db 3721 GGGCCAGCTTTTCTCACCAGGCGCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780  
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QY 3793 CCTGAT 3798  
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Db 3781 CCAGAT 3786  
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## RESULT 8

US-10-054-611-224  
; Sequence 224, Application US/10054611  
; Publication No. US20030059787A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Ligner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. US20030059787A1el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/054,611  
; FILING DATE: 18-Jan-2002  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/854,050  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 224:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4015 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA





QY 1993 CAGAACGTTCCGCAGAGAAAGAGGCGCGAGCGTCTCACCTCGAGGCTGAAGGCACGTGT 2052  
Db 1981 CAGAACGTTCCGCAGAGAAAGAGGCGCGAGCGTCTCACCTCGAGGCTGAAGGCACGTGT 2040  
QY 2053 CAGCGTCTCAACTACAGCGGGCGCGCGCGCGCGCGCGCTCTCGGGCGCTCTGTGCTGGG 2112  
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Db 2101 CCTGGAGATATCCACAGGCGCTGGGCGACCTTCTGCTGCTGCGGTGCGGGCCCGAGGACCC 2160  
QY 2173 GCSCCTGAGCTCTACTTCTCAAGGTGAGTGTGAGCGGGCGCTAGACACCATCCCCA 2232  
Db 2161 GCSCCTGAGCTCTACTTCTCAAGGTGAGTGTGAGCGGGCGCTAGACACCATCCCCA 2220  
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QY 2293 TCGGTATGCGGTGGTCCAGAAAGCGCGCCATGGGCACTGTCGCAAGGCCCTTCAAGAGCCA 2352  
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QY 2353 CGTCTTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGGCTCACTGCGAGGA 2412  
Db 2341 CGTCTTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGGCTCACTGCGAGGA 2400  
QY 2413 GACCAGCCGCTGAGGATGCGCTGCTATCGAGCAGAGCTCTCCCTGAATGAGGCCAG 2472  
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QY 2473 CAGTGGCCTTTCGACGTCTTCTACGCTTCATGTGCCACACGCGGTGGCATCAGGGG 2532  
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Db 2521 CAAGTCTAGCTCCAGTCCAGGGATCCCGCAGGCTCATCTCTCCAGCTGCTGCTG 2580  
QY 2593 CAGCCTGTGTACGGGCACATGGAGAACAGCTGTTTGGCGGGATTCGGCGGACGCGCT 2652  
Db 2581 CAGCCTGTGTACGGGCACATGGAGAACAGCTGTTTGGCGGGATTCGGCGGACGCGCT 2640  
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QY 2713 CTCTCTCAGGACCTTGTCGAGGTGTCCTGAGTATGGCTGCTGAGTTCGGAA 2772  
Db 2701 CTCTCTCAGGACCTTGTCGAGGTGTCCTGAGTATGGCTGCTGAGTTCGGAA 2760  
QY 2773 GACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCGCTTGGTGCGACGCGCTTTTGTTCAGAT 2832  
Db 2761 GACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCGCTTGGTGCGACGCGCTTTTGTTCAGAT 2820  
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QY 2893 GCAGAGGACTACTCCAGCTATCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2952  
Db 2881 GCAGAGGACTACTCCAGCTATCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG 2940  
QY 2953 CGGCTTCAAGGCTGGGAGGAACATGCGTCGAAACTCTTTGGGTCTTGGCGCTGAAGTG 3012  
Db 2941 CGGCTTCAAGGCTGGGAGGAACATGCGTCGAAACTCTTTGGGTCTTGGCGCTGAAGTG 3000  
QY 3013 TCACAGCCTGTTTCTGGATTTGCAAGTGAACAGCCTCCAGACGCTGTCACCAACATCTA 3072  
Db 3001 TCACAGCCTGTTTCTGGATTTGCAAGTGAACAGCCTCCAGACGCTGTCACCAACATCTA 3060  
QY 3073 CAAGATCCTCTCTCGAGCGGTACAGGTTTCAGGATGTGTCTCGAGCTCCCATTTCA 3132

Db 3061 CAAGATCCTCTCTGTCAGGCGTACAGSTTTACGCATGTGTGTCAGCTCCCATTTCA 3120  
QY 3133 TCAGCAAGTTTGGAAAGAACCCACATTTTCTCGCGTCTATCTCTGACAGGCGTCCCT 3192  
Db 3121 TCAGCAAGTTTGGAAAGAACCCACATTTTCTCGCGTCTATCTCTGACAGGCGTCCCT 3180  
QY 3193 CTGCTACTTCCATCCTGAAAGCAAGAACGACGAGGATGTGCTGGGGGCCAAGGGCGCGC 3252  
Db 3181 CTGCTACTTCCATCCTGAAAGCAAGAACGACGAGGATGTGCTGGGGGCCAAGGGCGCGC 3240  
QY 3253 CGGCGCTCTGCGCTCCAGAGCGGTGCAAGTGGCTGTGCACCAACATTTCTGCTCAAGCT 3312  
Db 3241 CGGCGCTCTGCGCTCCAGAGCGGTGCAAGTGGCTGTGCACCAACATTTCTGCTCAAGCT 3300  
QY 3313 GACTCGACACCGTGTCACTTACCTGACCTGCTGCGGTCTCTGAGGACAGCCAGAGCGCA 3372  
Db 3301 GACTCGACACCGTGTCACTTACCTGACCTGCTGCGGTCTCTGAGGACAGCCAGAGCGCA 3360  
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Db 3361 GCTGAGTCGGAAGCTCCCGGGGACGAGCTGACTGSCCTTGGAGGCCGAGCCACCGCGC 3420  
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QY 3553 CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCGCTGAGTGAAGTGTGGCGGAGGCGCTG 3612  
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Db 3601 CATGTCCGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGGAGTGTCCAGCCAAAGGCT 3660  
QY 3673 GAGTGTCCAGCACACCTGCGCTCTTACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA 3732  
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Db 3721 GGGCCAGCTTTTCTCACCAGGAGCCGCGGTTCACCTCCCCACATAGGAATAGTCCATCC 3780  
QY 3793 CCTGAT 3798  
Db 3781 CCAGAT 3786

RESULT 9  
US-10-105-963-1  
; Sequence 1, Application US/10105963  
; Publication No. US20030068818A1  
; GENERAL INFORMATION:  
; APPLICANT: Geron Corporation  
; APPLICANT: Denning, Chris  
; APPLICANT: Clark, A. John  
; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human  
; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection Syst  
; TITLE OF INVENTION: Recombination  
; FILE REFERENCE: 731/002  
; CURRENT APPLICATION NUMBER: US/10/105,963  
; CURRENT FILING DATE: 2002-03-21  
; PRIOR APPLICATION NUMBER: US 60/277,811  
; PRIOR FILING DATE: 2001-03-21  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 4015



[illegible]

Db 1981 CAGAACGTTCCGACAGAAAAAGAGGGCCGAGCGTCTCAACCTCGAGGGCTGAAGCACTGTT 2040  
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Db 2041 CAGCGTCTCAACTACAGCGGGGGCGGCGCCCGCGCTCTCTGCGGCCCTCTGTCGTGGG 2100  
QY 2113 CCTGGACGATATCCACAGGCGCTGGCGCACTTCGTGCTGGTGGCGGCCCGAGGACCC 2172  
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QY 2173 GCGCCCTGAGCTGTACTTTGTCAGGTGGATGTGACGGGCGGTACGACACCACTTCCGCCA 2232  
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Db 2581 CAGCGTGTGTCAGGGGACATGAGAACAAAGCTGTTTGGGGGATTCGGCGGAGCGGCT 2640  
QY 2653 GCTCCTCGGCTTGGTGATTTCTGTTGGTGACACCTCACTCACCCACCGGAAAC 2712  
Db 2641 GCTCCTCGGCTTGGTGATTTCTGTTGGTGACACCTCACTCACCCACCGGAAAC 2700  
QY 2713 CTTCTCTAGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCTGCTGAACTTGCAGAA 2772  
Db 2701 CTTCTCTAGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCTGCTGAACTTGCAGAA 2760  
QY 2773 GACAGTGGTGAACCTTCCTGTAGAACAGAGGCGCTGGGGGACGCGCTTTGTTTCAGAT 2832  
Db 2761 GACAGTGGTGAACCTTCCTGTAGAACAGAGGCGCTGGGGGACGCGCTTTGTTTCAGAT 2820  
QY 2833 GCGGGCCACGGGCTATTCCCTGTTGGCGGCTGCTGCTGATACCGGACCGCTGGAGGT 2892  
Db 2821 GCGGGCCACGGGCTATTCCCTGTTGGCGGCTGCTGCTGATACCGGACCGCTGGAGGT 2880  
QY 2893 GCAGCGGACTACTCCAGCTATCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG 2952  
Db 2881 GCAGCGGACTACTCCAGCTATCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG 2940  
QY 2953 CGGCTTCAAGCTGGGAGGAACATGCTGCCAACTCTTTGGGGTCTGGCGGTGAAGTG 3012  
Db 2941 CGGCTTCAAGCTGGGAGGAACATGCTGCCAACTCTTTGGGGTCTGGCGGTGAAGTG 3000  
QY 3013 TCACAGCTGTTTCTGATTTGAGGTGACGTTGACGCTTCCAGAGGCTGTCACCAACATCTA 3072  
Db 3001 TCACAGCTGTTTCTGATTTGAGGTGACGTTGACGCTTCCAGAGGCTGTCACCAACATCTA 3060  
QY 3073 CAAGATCCTCTGCTGCAGGCGTACAGGTTTACGCGATGTGCTGAGCTCCCATTTCA 3132  
Db 3061 CAAGATCCTCTGCTGCAGGCGTACAGGTTTACGCGATGTGCTGAGCTCCCATTTCA 3120

QY 3133 TCACGAAGTTTGGAAAGAACCCCACTTTTCTCTGCGGTCTATCTCTGACAGGGCTCCCT 3192  
Db 3121 TCACGAAGTTTGGAAAGAACCCCACTTTTCTCTGCGGTCTATCTCTGACAGGGCTCCCT 3180  
QY 3193 CTGCTACTCCTCTGAAAGCAAGAACGAGGATGCTGCTGGGGCCCAAGGGCGCGC 3252  
Db 3181 CTGCTACTCCTCTGAAAGCAAGAACGAGGATGCTGCTGGGGCCCAAGGGCGCGC 3240  
QY 3253 CCGCCCTCTGCGCTCCGAGGCGGTGACGTGGCTGTGCCAACCAAGCATTTCTGTCTCAAGCT 3312  
Db 3241 CCGCCCTCTGCGCTCCGAGGCGGTGACGTGGCTGTGCCAACCAAGCATTTCTGTCTCAAGCT 3300  
QY 3313 GACTCGACACCGTGTCACTTACCTTACGTGCGACCTCTCTGGGTCTACTCAGGACAGCCAGAGCA 3372  
Db 3301 GACTCGACACCGTGTCACTTACCTTACGTGCGACCTCTCTGGGTCTACTCAGGACAGCCAGAGCA 3360  
QY 3373 GCTCAGTCSGNAAGTCCCGGGGAGGAGCTGACTGCGCTGGAGCCGACGCCAACCCGCG 3432  
Db 3361 GCTGAGTCGGAAGCTCCCGGGGAGGAGCTGACTGCGCTGGAGCCGACGCCAACCCGCG 3420  
QY 3433 ACTGCCCTCAGACTTCAAGACCATCTCTGGACTGATGGCCACCCGCCACAGCCAGGCGCA 3492  
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTCTGGACTGATGGCCACCCGCCACAGCCAGGCGCA 3480  
QY 3493 GAGCAGACACAGAGCCCTGTACGCCGGGCTCTACGTCCCAAGGAGGAGGGCGGCG 3552  
Db 3481 GAGCAGACACAGAGCCCTGTACGCCGGGCTCTACGTCCCAAGGAGGAGGGCGGCG 3540  
QY 3553 CACACCCAGCGCCGACCGCTGGGAGTCTGAGGCTGAGTGGTGGCGGAGGCGCTG 3612  
Db 3541 CACACCCAGCGCCGACCGCTGGGAGTCTGAGGCTGAGTGGTGGCGGAGGCGCTG 3600  
QY 3613 CATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT 3672  
Db 3601 CATGTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGAGTGTCCAGCCAAAGGCT 3660  
QY 3673 GAGTGTCCAGCACACCTGCGCTTCTACTTCCCCACAGGCTGGGCTCGGCTCCACCCCA 3732  
Db 3661 GAGTGTCCAGCACACCTGCGCTTCTACTTCCCCACAGGCTGGGCTCGGCTCCACCCCA 3720  
QY 3733 GGGCAGCTTTTCTCTACAGGAGCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3792  
Db 3721 GGGCAGCTTTTCTCTACAGGAGCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780  
QY 3793 CCTGAT 3798  
Db 3781 CCAGAT 3786

RESULT 10

US-10-044-692-1  
; Sequence 1, Application US/10044692  
; Publication No. US20030096344A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.

; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND  
; THERAPEUTIC METHODS  
; NUMBER OF SEQUENCES: 335  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:













|||||  
Db 421 CCGTCCCAACAGGTGACCGTACCGACGACTGCGGGGAGCGGGGCGTGGGGGCTGCTGCTGCG 480  
Qy 493 CCGCGTGGGGAGGACGTGCTGCTGCTACCTGCTGGCACGCTGCGCGCTCTTTGCTGGGT 552  
Db 481 CCGCGTGGGGAGGACGTGCTGCTACCTGCTGGCACGCTGCGCGTNTTTGCTGCTGGT 540  
Qy 553 GCGTCCAGCTGGCGCTACACAGGTGTGCGGGCGCGCTGTACAGCTGCGCGCTGCCAC 612  
Db 541 GGNATCCAGCTGGCGCTACCAAGTGTGCGGGCGCGCTGTACAGCTGCGCGCTGCNAC 600  
Qy 613 TCAGGCGCGCGCGCGCACAGCTAGTGACACCCCGAAGCGTCTGGATGCGNACGGCG 672  
Db 601 TCAGGCGCGCGCGCGCACAGCTANTGGA - CCGGAANGCGTGGGAT - CCAACGGCG 658  
Qy 673 CTGGAACCATAGGCTCAGGAGGCGGGGTCGCCCTGGCGTGCAGACCCCGGGTGGAG 732  
Db 659 CTGGAACCATAGGCTCAGGAGGCGGGGTCGCCCTGGG - CTGCCACCCCGGGTGGAG 717  
Qy 733 GAGCGCGGGGAGTGCCAGCGGAAGTCTGCGGTGCGCAAGAGGCCCGAGGCGTGGCG 792  
Db 718 GAGCGCGGGGAGTGCCAGCGGAAGTCTGCGGTGCCAAGAGGCCCGAGGCGTGGCG 777  
Qy 793 TGCCCTGAGCGGAGCGGCGCGCTGGGCGAGGGTCTTGGGCCACCCGGCAGGAC 852  
Db 778 TGCCCTGAGCGGAGCGGCGCGCTGGGCGAGGGTCTTGGGCCACCCGGCAGGAC 837  
Qy 853 GCGTGGACCGAGTGACCGTGGTTCCTGCTGGGTGTACCTGCCAGACCCCGCGAAGAC 912  
Db 838 GCGTGGACCGAGTGACCGTGGTTCCTGCTGGGTGTACCTGCCAGACCCCGCGAAGAC 897  
Qy 913 CACCTCTTTGGAGGTCGCTCTGCGCAGCGCCACTCCCAACCATTCCTGCGGCGGCCA 972  
Db 898 CACCTCTTTGGAGGTCGCTCTGCGCAGCGCCACTCCCAACCATTCCTGCGGCGGCCA 957  
Qy 973 GCACGCGGGCGCGCGCATCCACATCGCGCGCACACGTCCTTGGGACAGCCTTCTCC 1032  
Db 958 GCACGCGGGCGCGCGCATCCACATCGCGCGCACACGTCCTTGGGACAGCCTTCTCC 1016  
Qy 1033 CCGGGTGTACGCGGAGACCAAGCACTTCTCTACTCTCAGGGGACAAAGGACAGCTGCG 1092  
Db 1017 CCGGGTGTACGCGGAGACCAAGCACTTCTCTACTCTCAGGGGACAAAGNA - CACTGCG 1074  
Qy 1093 GCGCTCTCTCTACTC - AGCTCTCTGAGGCGCGAGCTGACTGCGGCTCGGAGGTCGTGG 1151  
Db 1075 NCCTCTCTCTACTCAATATATCTGAGGCGCGAGCTGACTGCGGCTTCGGGAGTTCGTG 1134  
Qy 1152 AGACCATCTTCTGCGTTCAGGCGCTGATGCGAGGACTCCCGCAGGTCGCCCGCGC 1211  
Db 1135 GAGACANTCTTCTGCTTCCAGGCTTGGATGCCA - GGATTCGCCGAGGTTGCCCGCGC 1193  
Qy 1212 TGCCCCAGCGCTACTGGCAATCGGGCCCTGTTTCTGAGCTGCTTGGGAACCAACGCGC 1271  
Db 1194 TGCCCCAGCGNTACTGGCAATCGGGCCCTGTTTCTGAGCTGCTTGGGAACCAACGCGC 1253  
Qy 1272 AGTGCCCTTACGGGTCCTCTCAAGAGCACTGCCGCTGCGAGCTGCGGTCACCCAG 1331  
Db 1254 AGTGCCCTTACGGGTCCTCTCAAGAGCACTGCCGCTGCGAGCTGCGGTCACCCAG 1313  
Qy 1332 CAGCGGTGCTGTGCCCGGAGAACCCAGGCTCTGTGGCGGCCCGGAGGAGG 1391  
Db 1314 CAGCGGTGCTGTGCCCGGAGAACCCAGGCTCTGTGGCGGCCCGGAGGAGG 1373  
Qy 1392 - ACACAGACCCCGTCCCTGGTGCAGCTCTCCGCCAGCACAGACGCCCTGGCAGGTG 1450  
Db 1374 AACACAGACCCCGTCCCTGGTGCAGCTCTCCGCCAGCACAGACGCCCTGGCAGGTG 1433  
Qy 1451 TAGGGCTTGTGGGGCTGCTGCGCGGCTGGTGGCCCCAGGCTCTGGGGTCCAGG 1510  
Db 1434 TAGGGCTTGTGGGGCTGCTGCGCGGCTGGTGGCCCCAGGCTCTGGGGTCCAGG 1493  
Qy 1511 CACAACGACCGCTTCTCTCAGGAACACCAAGATTCATCTCCCTGGGGAGCATGCC 1570  
|||||

Db 1494 CACAACGAACGCCCTTCTCAGGAACACCAAGATTCATCTCCCTGGGGAAGCATGCC 1553  
Qy 1571 AAGCTCTCGCTGCAAGGACTGACGTGGAAGATGAGCGTGGGGACTGCGCTTGGCTGGC 1630  
Db 1554 AAGCTCTCGCTGCAAGGACTGACGTGGAAGATGAGCGTGGGGACTGCGCTTGGCTGGC 1613  
Qy 1631 AGGAGCCCAAGGGTGGCTGTGTTCGGGCCGAGAGCACCGCTCTGCGTAGAGATCCTG 1690  
Db 1614 AGGAGCCCAAGGGTGGCTGTGTTCGGGCCGAGAGCACCGCTCTGCGTAGAGATCCTG 1673  
Qy 1691 GCCAAGTTCCTGCACTGGCTGATGAGTGTGACGTCTGAGCTGCTGAGTCTTCTTT 1750  
Db 1674 GCCAAGTTCCTGCACTGGCTGATGAGTGTGACGTCTGAGCTGCTCAGTCTTCTTT 1733  
Qy 1751 TATGTCACGGAGACACGTTTCAAAAGAACAGGCTCTTTTTTCTACCGGAAGAGTCTGG 1810  
Db 1734 TATGTCACGGAGACACGTTTCAAAAGAACAGGCTCTTTTTTCTACCGGAAGAGTCTGG 1793  
Qy 1811 AGCAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTCGGGAGCTG 1870  
Db 1794 AGCAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTCGGGAGCTG 1853  
Qy 1871 TCGGAAGCAGAGGTCAGGACGATCGGGAGCCAGGCCCGCCCTGCTGACGCTCAGACTC 1930  
Db 1854 TCGGAAGCAGAGGTCAGGACGATCGGGAGCCAGGCCCGCCCTGCTGACGCTCAGACTC 1913  
Qy 1931 CGCTTCATCCCAAGCCTGACGGCTGCGGCCGATTTGTGAACATGGACTACGCTCGTGGGA 1990  
Db 1914 CGCTTCATCCCAAGCCTGACGGCTGCGGCCGATTTGTGAACATGGACTACGCTCGTGGGA 1973  
Qy 1991 GCCAGAAGCTTTCGAGAGAAAAGGGCCGAGGCTCTCACCTCGAGGGTGAAGSCACTG 2050  
Db 1974 GCCAGAAGCTTTCGAGAGAAAAGGGCCGAGGCTCTCACCTCGAGGGTGAAGSCACTG 2033  
Qy 2051 TTCAGCGTGTCAACTACGAGCGGCGGGGCCCGCCCTCTTGGGGCCCTCTGTGCTG 2110  
Db 2034 TTCAGCGTGTCAACTACGAGCGGCGGGGCCCGCCCTCTTGGGGCCCTCTGTGCTG 2093  
Qy 2111 GGCCTGGACGATATCCACAGGCGCTGCGCACTTCTGCTGCTGCTGCGGGCCAGGAC 2170  
Db 2094 GGCCTGGACGATATCCACAGGCGCTTGGCGCACTTCTGCTGCTGCTGCGGGCCAGGAC 2153  
Qy 2171 CCGCGCGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGCGGCTAGCACCATCCCC 2230  
Db 2154 CCGCGCGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGCGGCTAGCACCATCCCC 2213  
Qy 2231 CAGGACAGGCTCAGGAGGTCATCGCAGCATCATCAAAACCCAGAACACGCTACTGCGTG 2290  
Db 2214 CAGGACAGGCTCAGGAGGTCATCGCAGCATCATCAAAACCCAGAACACGCTACTGCGTG 2273  
Qy 2291 CGTCGCTATGCGGTGTCAGAGCGCGCCCATGGGACGCTCCGCAAGGCGCTTCAAGAGC 2350  
Db 2274 CGTCGCTATGCGGTGTCAGAGCGCGCCCATGGGACGCTCCGCAAGGCGCTTCAAGAGC 2333  
Qy 2351 CAGCTCTTACCTTGACAGACCTCCAGCGGTACATGGGACAGTTCGTGGGTCACCTGCGAG 2410  
Db 2334 CAGCTCTTACCTTGACAGACCTCCAGCGGTACATGGGACAGTTCGTGGGTCACCTGCGAG 2393  
Qy 2411 GAGACACCGCGCTGAGGATGCGTCTATCGAGCAGAGCTCTCCCTCAAGTAGGCGC 2470  
Db 2394 GANAACAGCGCGTGGGATGCGTCTATCGAGCAGAGCTCTCTCCCTCAAGTAGGCGC 2453  
Qy 2471 AGCAGTGGCGCTTTCGACGCTTCTTACGCTTTCATGTGCCACACGCGCTCGCATCAGG 2530  
Db 2454 AGCAGTGGCGCTTTCGACGCTTCTTACGCTTTCATGTGCCACACGCGCTCGCATCAGG 2513  
Qy 2531 GGCAGTCTTACGTCAGTCCAGTGGCAGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTC 2590  
Db 2514 GGCAGTCTTACGTCAGTCCAGTGGCAGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTC 2573  
Qy 2591 TGCAGCCTGTGCTACGCGGACATGGAACAAAGCTTTTGGGGGATTCGCGGGAGCGG 2650  
Db 2574 TGCAGCCTGTGCTACGCGGACATGGAACAAAGCTGTTTTGGGGGATTCGCGGGAGCGG 2633





OTHER INFORMATION: human TRF cDNA insert of  
OTHER INFORMATION: plasmid pGRN121\*  
US-09-438-486-173

Query Match 95.3%; Score 3618.6; DB 11; Length 4029;  
Best Local Similarity 98.3%; Pred. No. 0;  
Matches 3725; Conservative 0; Mismatches 54; Indels 9; Gaps 8;

Qy	13	GCAGCGTGGCTGCTGTCGCGACAGTGGGAAGCCCTGGCCCGCCACCCCGCGATGCC	72
Db	1	GCAGCGTGGCTGCTGTCGCGACAGTGGGAAGCCCTGGCCCGCCACCCCGCGATGCC	60
Qy	73	CGCGCTCCCGCTGCGGAGCGCTGCGCTCCCTGCTCGCGACGACATACCGCGAGTGC	132
Db	61	CGCGCTCCCGCTGCGGAGCGCTGCGCTCCCTGCTCGCGACGACATACCGCGAGTGC	120
Qy	133	CGCGCTGGCCACGTTCTGCGGGGCGCTGGGGCCCGCCAGGCTGGCGGTGGTGCAGCGCG	192
Db	121	CGCGCTGGCCACGTTCTGCGGGGCGCTGGGGCCCGCCAGGCTGGCGGTGGTGCAGCGCG	180
Qy	193	GGACCGCGGCGTTTCCGCGCGTGGTGGCCAGTGCCTGGTGGTGCCTGGGACGC	252
Db	181	GGACCGCGGCGTTTCCGCGCGTGGTGGCCAGTGCCTGGTGGTGCCTGGGACGC	240
Qy	253	ACGGCCCGCCCGCGCCCGCTTCCGCGCGAGTGTCCGCGAGTGTCTGCTGAAGAGCTGGTGC	312
Db	241	ANGCNCGCCCGCCCGCCCGCTTCCGCGCGAGTGTCTGCTGAAGAGTGGTGGC	300
Qy	313	CCGAGTGTGCAGAGGTTGTCGAGCGCGCGCGGAAGAGTGTGCGCTTCCGCTTCGC	372
Db	301	CCGAGTGTGCANAGCTGTGCGANCGCGCGCGGAANAAGTGTGCTGGCTTCGC	360
Qy	373	GCTGCTGGAGGGCGCGCGGGGCGCCCGAGGCGCTTACCACACAGCTGGCGAGCTA	432
Db	361	GCTGCTGGAGGGCGCGCGGGGCGCCCGAGGCGCTTACCACACAGCTGGCGAGCTA	420
Qy	433	CTTGCCCAACACAGTGTACACAGCTGCGCGGAGCGGCGGTGGGGGCTGCTGTCGC	492
Db	421	CTTGCCCAACACAGTGTACACAGCTGCGCGGAGCGGCGGTGGGGGCTGCTGTCGC	480
Qy	493	CCGCGTGGGCGAGCAGTGTGTTTACCTGCTGCGACAGCTGCGCGCTCTTTTGTGCTGT	552
Db	481	CCGCGTGGGCGAGCAGTGTGTTTACCTGCTGCGACAGCTGCGCGCTCTTTTGTGCTGT	540
Qy	553	GGCTCCAGCTGGCGCTACAGTGTGCGGGCGCGCGCTGTACAGCTCGCGGTGCGCAC	612
Db	541	GGTCCAGCTGGCGCTTACAGTGTGCGGGCGCGCGCTGTACAGCTCGCGGTGCGCAC	600
Qy	613	TCAGGCCCGCCCGCCGACACAGCTAGTGGACCCCGAAGCGCTGCGGATGCCAGCGGC	672
Db	601	TCAGGCCCGCCCGCCGACACAGCTAGTGGACCCCGAAGCGCTGCGGATGCCAGCGGC	658
Qy	673	CTGGAACATAGCGTCAGGAGCGCGGGTCCCGCTGGGCTGCGAGCCCGGGTGGAG	732
Db	659	CTGGAACATAGCGTCAGGAGCGCGGGTCCCGCTGGG-CTGCCAGCCCGGGTGGAG	717
Qy	733	GAGGCGGGGCGAGTGCAGCGAAGTCTGCCCTTGCACAGAGGCCCGAGCGTGGCGC	792
Db	718	GAGGCGGGGCGAGTGCAGCGAAGTCTGCCCTTGCACAGAGGCCCGAGCGTGGCGC	777
Qy	793	TGCCCCGTAGCCGGAGCGAGCCCGTGGGCGAGGGTCTTGGGCCACCCGGCGAGAC	852
Db	778	TGCCCCGTAGCCGGAGCGAGCCCGTGGGCGAGGGTCTTGGGCCACCCGGCGAGAC	837
Qy	853	CGCTGGACAGTGAACGCTGTTCTGCTGCTGCTACCTGCCAGACCCCGCGAAGAC	912
Db	838	CGCTGGACAGTGAACGCTGTTCTGCTGCTGCTACCTGCCAGACCCCGCGAAGAC	897
Qy	913	CACCTCTTTGGAGGGTGCCTCTCTGGCACGCGCCACTCCACCCATCCGTTGGCGCGCA	972
Db	898	CACCTCTTTGGAGGGTGCCTCTCTGGCACGCGCCACTCCACCCATCCGTTGGCGCGCA	957
Qy	973	GCACCGCGGGGCCCCCATCCACATCGCGGGCCACCACTGCCCTTGGGACAGCGCTGTCC	1032

Db	958	GCACCGCGGGGCCCCCATCCACATCGCGGCCACACGT-CTTGGGACACGCTTGTCC	1016
Qy	1033	CCCGGTGTACCGCGGAGACCAAGCACTTCTTACTCTCTCAGCGACGACGAGTGTCCG	1092
Db	1017	CCCGGTGTACCGCGGAGACCAAGCACTTCTTACTCTCTCAGCGACGACGAGTGTCCG	1074
Qy	1093	GCCCTCTCTCTTACTC-AGCTCTCTGAGGCCAGCTGACCTGGGCTCGGAGGTCGNG	1151
Db	1075	NCCCTCTCTCTTACTCAATATATCTGAGGCCAGCTGACCTGGGTTCGGAGGTCGTG	1134
Qy	1152	AGACCATCTTCTTCTGGGTTCCAGGCCCTGGATGCCAGGACCTCCCGCAGTGTGCCGCC	1211
Db	1135	GAGACANTCTTCTTCTGGTTCCAGGCTTGGATGCCA-GGATTCGCCGAGTGTGCCGCC	1193
Qy	1212	TGCCCGAGCGCTACTTGGCAATGCGGCCCTTCTTCTTCTTGGAGCTGCTTGGGACCA	1271
Db	1194	TGCCCGAGCGTACTTGGCAATGCGGCCCTTCTTCTTCTTGGAGCTGCTTGGGAA	1253
Qy	1272	AGTCCCGCTACGGGTGCTCTCAAGAGCACTGCCCGCTCGAGCTCGGTCACCCCGAG	1331
Db	1254	AGTCCCGCTACGGGTGCTCTCAAGAGCACTGCCCGCTCGAGCTCGGTCACCCCGAG	1313
Qy	1332	CAGCGGTGCTGTGCCCGGAGAACGCCAGGGCTCTGTGGCGGCCCGCCAGGAGG	1391
Db	1314	CAGCGGTGCTGTGCCCGGAGAACGCCAGGGCTCTGTGGCGGCCCGCCAGGAGG	1373
Qy	1392	-ACACAGACCCCGCTGCGCTGTCAGTGTCTCCCGCAGGCTGCGGGTTCACAG	1450
Db	1374	AACACAGACCCCGCTGCGCTGTCAGTGTCTCCCGCAGGCTGCGGGTTCACAG	1433
Qy	1451	TACGGCTTCTGTGGCGGCTGCTGCGCGGCTGCTGCGGCCAGGCTTGGGGTTCACAG	1510
Db	1434	TACGGCTTCTGTGGCGGCTGCTGCGCGGCTGCTGCGGCCAGGCTTGGGGTTCACAG	1493
Qy	1511	CACAAACAGCCCGCTTCTCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGCATGCC	1570
Db	1494	CACAAACAGCCCGCTTCTCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGCATGCC	1553
Qy	1571	AAGCTCTCGCTGCGAGGCTGACGTGAAGATGAGCTGCGGGACTGCGCTTGTGCTGGC	1630
Db	1554	AAGCTCTCGCTGCGAGGCTGACGTGAAGATGAGCTGCGGGACTGCGCTTGTGCTGGC	1613
Qy	1631	AGGAGCCAGGGTGTGTTTCCGGCCGAGACACCGCTCTCGGTGAGGATGCTG	1690
Db	1614	AGGAGCCAGGGTGTGTTTCCGGCCGAGACACCGCTCTCGGTGAGGATGCTG	1673
Qy	1691	GCCAGTTCCTGCACTGGCTGATGATGATGATGATGATGATGATGATGATGATGATG	1750
Db	1674	GCCAGTTCCTGCACTGGCTGATGATGATGATGATGATGATGATGATGATGATGATG	1733
Qy	1751	TATGTCAGGAGACACGTTTCAAAAGAACAGGCTCTTTTCTTACCGGAAGAGTCTCG	1810
Db	1734	TATGTCAGGAGACACGTTTCAAAAGAACAGGCTCTTTTCTTACCGGAAGAGTCTCG	1793
Qy	1811	AGCAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGTCAGCTCGGGAGCTG	1870
Db	1794	AGCAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGTCAGCTCGGGAGCTG	1853
Qy	1871	TCGGAACGAGGTCAGGAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCAGACTC	1930
Db	1854	TCGGAACGAGGTCAGGAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCAGACTC	1913
Qy	1931	CGCTTCATCCCAAGCTGCGGGCTGCGGCCGATTTGTGAACATGGACTAGCTCGTGGGA	1990
Db	1914	CGCTTCATCCCAAGCTGCGGGCTGCGGCCGATTTGTGAACATGGACTAGCTCGTGGGA	1973
Qy	1991	GCCAGAACGTTTCCGAGAGAAAGAGGCCCGAGGCTCTCAGCTCGAGGTCAGGCACTG	2050
Db	1974	GCCAGAACGTTTCCGAGAGAAAGAGGCCCGAGGCTCTCAGCTCGAGGTCAGGCACTG	2033
Qy	2051	TTGAGCGTGTCAACTACGAGCGGGCGGGCGGCCCTTCTTGGGCGCTCTGTGTCT	2110

2034	Db	TTCCAGCGTGTCTAACTACAGAGCGGGCGGGCGCCCGGCGCTCTCTGGGGCGCTCTGTGTGCTG	2099
2111	QY	GGCCTTGGACGATATCCACAGGGGCTTGGCGCACCTTCGTGTGTGTGTGGGGGCCACAGGAC	2170
2094	Db	GGCCTTGGACGATATCCACAGGGGCTTGGCGCACCTTCGTGTGTGTGTGGGGGCCACAGGAC	2153
2171	QY	CCGCGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGGCGGTACGACACCATTCCTCC	2230
2154	Db	CCGCGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGGCGGTACGACACCATTCCTCC	2213
2231	QY	CAGGACAGGCTCAGGAGGTTCATCGCCAGCATCATCAAAACCCACAGAACCATGACTTCGGTG	2290
2214	Db	CAGGACAGGCTCAGGAGGTTCATCGCCAGCATCATCAAAACCCACAGAACCATGACTTCGGTG	2273
2291	QY	CGTCGCTATGCCGTGTCCAGAAAGCGGCCCATGGCAGCTCCGCAAGGCGCTTCAAGAGC	2350
2274	Db	CGTCGCTATGCCGTGTCCAGAAAGCGGCCCATGGCAGCTCCGCAAGGCGCTTCAAGAGC	2333
2351	QY	CAGCTCTCTACCTTTGACAGACCTCCAGCGGTACATCGGACAGTTCTGTGGCTCACCTGCAG	2410
2334	Db	CAGCTCTCTACCTTTGACAGACCTCCAGCGGTACATCGGACAGTTCTGTGGCTCACCTGCAG	2393
2411	QY	GAGACACGCCGCTGAGGATGCGCTGTCTATCGAGCAGAGCTCTCTCTGTAATGAGGC	2470
2394	Db	GANAACAGCCGCTGAGGATGCGCTGTCTATCGAGCAGAGCTCTCTCTGTAATGAGGC	2453
2471	QY	AGCAGTGGGCTCTTCGACAGCTCTTCCTACGCTTTCATGTGCCACACCGCTGGCGCATCAG	2530
2454	Db	AGCAGTGGGCTCTTCGACAGCTCTTCCTACGCTTTCATGTGCCACACCGCTGGCGCATCAG	2513
2531	QY	GGCAAGTCTACGTCAGTGCAGAGGGATGCCGAGGGCTCCATCTCTCTCAGCGTGCCTC	2590
2514	Db	GGCAAGTCTCTACGTCAGTGCAGAGGGATGCCGAGGGCTCCATCTCTCTCAGCGTGCCTC	2573
2591	QY	TGCAGCGCTGTGCTACGCGACATGTGAGAACAAAGCTGTTTGCGGGGATTCGGCGGGACGG	2650
2574	Db	TGCAGCGCTGTGCTACGCGACATGTGAGAACAAAGCTGTTTGCGGGGATTCGGCGGGACGG	2633
2651	QY	CTGCTCCTGGTTTGGTGATATTCCTTGTGGTGACACCTCACCTCACCCACGCGGAAA	2710
2634	Db	CTGCTCCTGGTTTGGTGATATTCCTTGTGGTGACACCTCACCTCACCCACGCGGAAA	2693
2711	QY	ACCTTCTCAGGACCTGTGTCGAGGTGTCCTCTGAGTATGGGTCGCTGTGTAACCTTTCGG	2770
2694	Db	ACCTTCTCAGGACCTGTGTCGAGGTGTCCTCTGAGTATGGGTCGCTGTGTAACCTTTCGG	2753
2771	QY	AAGCAGTGTGTAACCTCCCTGTAGAGAGCAGGCGCTGGTGGCAGCGCTTTGTGTCAG	2830
2754	Db	AAGCAGTGTGTAACCTCCCTGTAGAGAGCAGGCGCTGGTGGCAGCGCTTTGTGTCAG	2813
2831	QY	ATGCGGGCCACAGGCTATTCCCTGTGTGGGGGCTGTCTGTGATACCGGACCCCTGGAG	2890
2814	Db	ATGCGGGCCACAGGCTATTCCCTGTGTGGGGGCTGTCTGTGATACCGGACCCCTGGAG	2873
2891	QY	GTGACAGAGCACTACTCCAGCTATGCCGGACCTCCATCAGAGGCCAGTCTCACTTCAAC	2950
2874	Db	GTGACAGAGCACTACTCCAGCTATGCCGGACCTCCATCAGAGGCCAGTCTCACTTCAAC	2933
2951	QY	CGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTTGGCGCTGAAG	3010
2934	Db	CGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTTGGCGCTGAAG	2993
3011	QY	TGTCACAGCCTGTTTCTGGATTTCGAGGTGAACAGCCTCCAGACGGTGTGCAACCAATC	3070
2994	Db	TGTCACAGCCTGTTTCTGGATTTCGAGGTGAACAGCCTCCAGACGGTGTGCAACCAATC	3053
3071	QY	TACAAGATCCTCTGTGTGACGGGCTACAGGTTTTCACGCGCATGTGTGCTGCAGCTCCCATTT	3130
3054	Db	TACAAGATCCTCTGTGTGACGGGCTACAGGTTTTCACGCGCATGTGTGCTGCAGCTCCCATTT	3113
3131	QY	CATCAGCAAGTTTGGAGAACCCCAATTTTTTCTGGGGGTCACTCTGCACAGGCGCTCC	3190
3114	Db	CATCAGCAAGTTTGGAGAACCCCAATTTTTTCTGGGGGTCACTCTGCACAGGCGCTCC	3173

QY	3191	CTCTGCTACTCTCATCTCTGTAAGCCAGCAAGCGCAGGGATGTCTGTGGGGGCCAAGGGCGCC	3250
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Db	3414	GCCTGCCCCTCAGACTTTCAGAGCACCCTCTGGACTGTATGGCCACCCGCCACAGCCAGAGCC	3473
QY	3491	GAGAGCAGACACACAGAGCCCTGTACGCCCGGGCTCTACGTCCAGGGAGGGAGGGGCGG	3550
Db	3474	GAGAGCAGACACACAGAGCCCTGTACGCCCGGGCTCTACGTCCAGGGAGGGAGGGGCGG	3533
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## RESULT 14

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; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;           Lingner, Joachim
;           Nakamura, Toru
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;           Morin, Gregg B.
;           Harley, Calvin
;           Andrews, William H.
; TITLE OF INVENTION: NO. US20030032075A1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
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APPLICATION NUMBER: US/08/851,843  
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APPLICATION NUMBER: US/08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US/08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 173:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4029 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: LOCATION: 1..4029  
OTHER INFORMATION: /note= "preliminary sequence for human Trk cDNA insert of plasmid pGRN121"  
SEQUENCE DESCRIPTION: SEQ ID NO: 173:  
US-10-053-758-173

Query Match 95.38; Score 3618.6; DB 14; Length 4029;  
Best Local Similarity 98.3%; Pred. No. 0;  
Matches 3725; Conservative 0; Mismatches 54; Indels 9; Gaps 8;  
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DB 61 GCGGCTCCCGCTGCGCAGCGCTGCGCTCCCTGCTGCGCAGCCTACCGCAGAGTGC 120  
QY 133 GCGGCTGGCCAGCTGCTGCGGCGCCTGGGGCCCCAGGGCTGGGGCTGGCAGCGG 192  
DB 121 GCGGCTGGCCAGCTGCTGCGGCGCCTGGGGCCCCAGGGCTGGGGCTGGCAGCGG 180  
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QY 253 ACGGCGCGCGCGCGCGCGCGCTTCCCTCCCGCAGGTGCTTCCCGCAGGTGCTGGC 312  
DB 241 ANGCGCGCGCGCGCGCGCGCTTCCCGCAGGTGCTTCCCGCAGGTGCTTCCGANGN 300  
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QY 1571 AAGCTCTCGCTGAGGAGCTGAGCGTGGAGAGTGAAGCGTGGGGGACTGCGCTTGGCTGCG 1630

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Qy	1931		CGCTTCATCCCCAAGCCTGACGGGCTCGGGCCGATTTGTGAACATGACGTACGTCTGGGA	1990
Db	1914		CGCTTCATCCCCAAGCCTGACGGGCTCGGGCCGATTTGTGAACATGACGTACGTCTGGGA	1873
Qy	1991		GCCAGAAGCTTCCACAGAAAGAGAGGCCGAGGCTCTCACTCCAGAGGTGAAGGCACTG	2050
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Db	1374	ACACAGACCCCGCTCGCCTGGTGTGAGCTGTCTCCGCCACACAGACGCCCTGGCAGGTG	1433
QY	1451	TACGGCTTCGTGCGGGCTTCCTGCGCCGGCTGGTGCCTCCAGGCCCTCTGGGGCTCCAGG	1510
Db	1434	TACGGCTTCGTGCGGGCTTCCTGCGCCGGCTGGTGCCTCCAGGCCCTCTGGGGCTCCAGG	1493
QY	1511	CACACGAACGGCGCTCTCTAGGAACACCAAGAGTTTCATCTCCCTGGGGAGCATGCC	1570
Db	1494	CACACGAACGGCGCTCTCTAGGAACACCAAGAGTTTCATCTCCCTGGGGAGCATGCC	1553
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Db	1554	AAGCTCTCGCTCAGGAGCTGACGTGGAAGATGAGCTGCGGAGCTGCGCTGGCTGGCG	1613
QY	1631	AGGAGCCCAAGGGTGGCTGTCTCCGGCCGAGAGCACCGTCTGCGTGAGGAGATCCCTG	1690
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QY	1811	AGCAAGTTCGAAGCATTGGAAATCAGACAGCACTTGAAGAGGCTGAGCTGCGGGAGCTG	1870
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Db	1914	CGCTTCATCCCAAGCTGACGGCTGCGGCCGATGTGAACATGACTACCTCGTGGA	1973
QY	1991	GGCAGAACCTTCGCGAGAGAAAGAGGGCCGAGCGCTCACCTCGAGGCTGAAGGCATG	2050
Db	1974	GGCAGAACCTTCGCGAGAGAAAGAGGGCCGAGCGCTCACCTCGAGGCTGAAGGCATG	2033
QY	2051	TTACAGGCTCTCAACTACAGGGGGCGGCCGCCGCCCTCCTGGGCCCTCTGTGCTG	2110
Db	2034	TTACAGGCTCTCAACTACAGGGGGCGGCCGCCGCCCTCCTGGGCCCTCTGTGCTG	2093
QY	2111	GGCCTTGGAGATATCCACAGGGCTTGGGCCACCTTCGTGCTGCTGGGGCCCAAGGAC	2170
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Db	2154	CGCGCCCTTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGGCGCTTACACACCATCCOC	2213
QY	2231	CAGGACAGGCTCAGGAGGTCAATCGCCAGCATCATCAAAACCCAGAACAGTACTCGGTG	2290
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Db	2274	CGTCGGTATGCGGTGCTCCAGAGGCGCCCATGGCAGCTCGCGAAGGCCCTTCAAGAGC	2333
QY	2351	CACGTCTTACCTTGACAGACCTCCAGCGGTACATCGACAGTTCGTGGCTCACCTGCAG	2410
Db	2334	CACGTCTTACCTTGACAGACCTCCAGCGGTACATCGACAGTTCGTGGCTCACCTGCAG	2393
QY	2411	GAGACAGCCCGCTGAGGGATGCCGTGCTCATGCGACAGAGTCTCTCCCTGAATGAGGCC	2470
Db	2394	GANAACAGCCCGCTGAGGGATGCCGTGCTCATGCGACAGAGTCTCTCCCTGAATGAGGCC	2453
QY	2471	AGCAGTGGGCTCTTTCAGCGTCTTCTTACGCTTCATGCGCACACCGCTGGCCATCAGG	2530
Db	2454	AGCAGTGGGCTCTTTCAGCGTCTTCTTACGCTTCATGCGCACACCGCTGGCCATCAGG	2513
QY	2531	GGCAAGTCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCTCTCCAGGCTGCTC	2590
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QY	2651	CTGCTCTCGCTTGGTGGATGATTTCTTGTGTTGTTGACACCTCACCTCACCCACGGGAA	2710
Db	2634	CTGCTCTCGCTTGGTGGATGATTTCTTGTGTTGTTGACACCTCACCTCACCCACGGGAA	2693
QY	2711	ACCTTCTCAGAACCTTGTGCGAGGTGCTCCCTGAGTATGGTGTGCTGTAACCTTGCAG	2770
Db	2694	ACCTTCTCAGAACCTTGTGCGAGGTGCTCCCTGAGTATGGTGTGCTGTAACCTTGCAG	2753
QY	2771	AGACAGTGTGTAACCTTCCCTGTAGAGACAGAGGCCCTGGTGGGACGGCTTTTGTTCAG	2830
Db	2754	AGACAGTGTGTAACCTTCCCTGTAGAGACAGAGGCCCTGGTGGGACGGCTTTTGTTCAG	2813
QY	2831	ATGCCGGCCACAGGCCCTATTCCTCGTGGGCTGCTGCTGGATACCGGACCCCTGGAG	2890
Db	2814	ATGCCGGCCACAGGCCCTATTCCTCGTGGGCTGCTGCTGGATACCGGACCCCTGGAG	2873
QY	2891	GTGACAGGAGTACTTCCAGCTATGCCCGAACCTCCATCAGAGCCAGTCTCACCTTCAAC	2950
Db	2874	GTGACAGGAGTACTTCCAGCTATGCCCGAACCTCCATCAGAGCCAGTCTCACCTTCAAC	2933
QY	2951	CGGGGCTTCAAGGCTGGGAGAACATGCGTCCGAAACTCTTTGGGGTCTTGGGGCTGAAG	3010
Db	2934	CGGGGCTTCAAGGCTGGGAGAACATGCGTCCGAAACTCTTTGGGGTCTTGGGGCTGAAG	2993
QY	3011	TGTCACAGCTGTTCCTGATTTGCAAGGTGAACAGCTCCAGAGCTGTCACCAACATC	3070
Db	2994	TGTCACAGCTGTTCCTGATTTGCAAGGTGAACAGCTCCAGAGCTGTCACCAACATC	3053
QY	3071	TACAAGTCTCTGCTGACGGCTACAGGTTTACGCATGTGTGCTGACAGTCTCCCATTT	3130
Db	3054	TACAAGTCTCTGCTGACGGCTACAGGTTTACGCATGTGTGCTGACAGTCTCCCATTT	3113
QY	3131	CATCAGAAAGTTTGAAGAACCCCATTTTTTCTCGGGCTCATCTCTGACAGGGCTCC	3190
Db	3114	CATCAGAAAGTTTGAAGAACCCCATTTTTTCTCGGGCTCATCTCTGACAGGGCTCC	3173
QY	3191	CTCTGCTACTTCCATCTCTGAAGAACAGGAGGATGCTGCTGGGGCCAGAGGGGCC	3250
Db	3174	CTCTGCTACTTCCATCTCTGAAGAACAGGAGGATGCTGCTGGGGCCAGAGGGGCC	3233
QY	3251	GGCGGGCTCTGCGCTCCGAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3310
Db	3234	GGCGGGCTCTGCGCTCCGAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3293



